IDENTIFYING DRUGS FOR AND DIAGNOSIS OF BENIGN PROSTATIC HYPERPLASIA USING GENE EXPRESSION PROFILES

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RELATED APPLICATIONS

This application claims priority of U.S. Provisional Application No. 60/223,323, filed August 7, 2000, and U.S. Application No. 09/873,319, filed June 5, 2001, which are herein incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

Benign Prostatic Hyperplasia (BPH) is the most common benign tumor in men aged >60 years. It is estimated that one in four men living to the age of 80 will require treatment for this disease. BPH is usually noted clinically after the age of 50, the incidence increasing with age, but as many as two thirds of men between the ages of 40 and 49 demonstrate histological evidence of the disease.

The anatomic location of the prostate at the bladder neck enveloping the urethra plays an important role in the pathology of BPH, including bladder outlet obstruction. Two prostate components are thought to play a role in bladder outlet obstruction. The first is the relative increased prostate tissue mass. The second component is the prostatic smooth muscle tone.

The causative factors of BPH in man have been intensively studied. See Ziada *et al.*, *Urology*, 53: 1-6, 1999. In general, the two most important factors appear to be aging and the presence of functional testes. Although these factors appear to be key to the development of BPH, both appear to be nonspecific.

Little is known about the molecular changes in prostate cells associated with the development and progression of BPH. It has been demonstrated that the expression levels of a number of individual genes are changed compared to normal prostate cells. These changes in gene expression include decreased expression of Wilm's tumor gene (WT-1) and increased expression of insulin growth factor II (IGF-II) (Dong *et al.*, *J. Clin. Endocrin. Metab.*, 82(7): 2198-220).

While the changes in the expression levels of a number of individual genes have been identified, the investigation of the global changes in gene expression has not been reported. Accordingly, there exists a need for the investigation of the changes in global gene expression levels as well as the need for the identification of new molecular markers associated with the development and progression of BPH. Furthermore, if intervention is expected to be successful in halting or slowing down BPH, means of accurately assessing the early manifestations of BPH need to be established. One way to accurately assess the early manifestations of BPH is to identify markers which are uniquely associated with disease progression. Likewise, the development of therapeutics to prevent or stop the progression of BPH relies on the identification of genes responsible for BPH growth and function.

SUMMARY OF THE INVENTION

The present invention is based on the elucidation of the global changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue as well as the identification of individual genes that are differentially expressed in BPH tissue.

The invention is also based on the discovery of a means of effectively selecting disease-linked drug targets from gene expression results. The invention includes methods of classifying genes whose expression levels are changed in diseased tissues, during disease induction or during disease progression into specific groups. By using this method it is possible to classify genes whose expression are regulated by the same mechanism into the same group, and it is possible to identify representative marker genes by selecting typical genes from each cluster.

The invention includes methods of screening for or identifying an agent that modulates the onset or progression of BPH, comprising: preparing a first gene expression profile of BPH cells; exposing the cells to the agent; preparing a second gene expression profile of the agent exposed cells; and comparing the first and second gene expression profiles. In a preferred embodiment of these methods, the gene expression profile comprises the expression levels of one or more or preferably two or more genes in Tables 1-6. In another preferred embodiment of these methods, the cell is a prostate cell from a BPH patient, a cell line in Table 7, or a derivative thereof.

The invention also includes methods of monitoring a treatment of a patient with BPH, comprising administering a pharmaceutical composition to the patient; preparing a gene expression profile from a prostate cell or tissue sample from the patient; and comparing the patient gene expression profile to a gene expression profile from a normal prostate cell population, a BPH tissue or BPH cells without treatment with the pharmaceutical composition. In preferred embodiments of these methods, the gene expression profile comprises the expression levels of one or more or, preferably two or more genes in Tables 1-6.

The invention also includes methods of diagnosing benign prostatic hyperplasia (BPH) in a subject comprising the step of detecting the level of expression in a tissue or cell sample from the subject of two or more genes from Tables 1-6 (preferably Tables 3-5, and more preferably Table 5); wherein differential expression of the genes is indicative of BPH progression.

The invention further includes methods of detecting the onset or progression of benign prostatic hyperplasia (BPH) in a patient comprising the step of detecting the level of expression in a tissue or cell sample of two or more genes from Tables 1-6 (preferably Tables 3-5, and more preferably Table 5); wherein differential expression of the genes is indicative of BPH progression.

The invention also includes methods of differentiating benign prostatic hyperplasia (BPH) from prostate cancer in a patient comprising the step of detecting the level of expression in a tissue or cell sample of two or more genes from Tables 1-6 (preferably Tables 3-5, and more preferably Table 5); wherein differential expression of the genes is indicative of BPH rather than prostate cancer.

The invention also includes methods of selecting or identifying cells that can be used for drug screening.

All of these methods may include the step of detecting the expression levels of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10 or more genes in any of Tables 1-6, or preferably Table 5. In a preferred embodiment, expression of all of the genes or nearly all of the genes in Tables 1-6, or preferably Table 5, may be detected.

The invention further includes sets of at least two or more probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-6 as well as solid supports comprising at least two or more of the probes.

The invention also includes computer systems comprising or linked to a database containing information identifying the expression level in BPH tissue or cells of a set of genes comprising at least two genes in Tables 1-6, preferably from Table 5; and a user interface to view the information. The database may further comprise sequence information for the genes as well as information identifying the expression level for the set of genes in normal prostate tissue or cells, and prostate cancer tissue. The database may further contain or be linked to descriptive information from an external database, which information correlates said genes to records in the external database.

The invention further includes methods of using the disclosed computer systems to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one of the genes in Tables 1-6, preferably Table 5, comprising comparing the expression level of at least one gene in Tables 1-6, preferably Table 5, in the tissue or cell to the level of expression of the gene in the database.

Lastly, the invention includes kits comprising probes or solid supports of the invention. In some embodiments, the kits also contain written materials or software concerning gene expression information for the genes of the invention, preferably in electronic format.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Figure 1 shows the expression of cellular retinol binding protein RNA in various tissues.

Figure 2. Figure 2 shows the expression of cellular retinol binding protein RNA in various prostate tissues samples. In all of the figures, "Normal", "-Sym", "Cancer" and "+Sym" refer to normal prostate, BPH without symptoms, prostate cancer, and BPH with symptoms, respectively.

Figure 3. Figure 3 shows the expression of S100 calcium binding protein RNA in various tissues.

Figure 4. Figure 4 shows the expression of S100 calcium binding protein RNA in various prostate tissue samples.

Figure 5. Figure 5 shows the expression of human prostate-specific membrane antigen (PSMA) RNA in various tissues.

Figure 6. Figure 6 shows the expression of PSMA RNA in various prostate tissue samples.

Figure 7A-7C. Figure 7A shows a 3-dimensional view of the results of a Preferred Component Analysis (PCA) comparing BPH patients with symptoms (S), asymptomatic BPH patients (O), asymptomatic BPH patients with prostate cancer (C) and normal control subjects (N). Figure 7B shows the same PCA in a 2-dimensional format plotting component 1 versus components 2+3. The patients are depicted here as: BPH patients with symptoms (BPHWS), asymptomatic BPH patients (BPHNoS), asymptomatic BPH patients with prostate cancer (Cancer) and normal control subjects (Normal). Figure 7C depicts the same data as Figure 7B, with the addition of two additional normal (Norm) and three additional BPH patients with symptoms (BPH).

DETAILED DESCRIPTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.* through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes could lead to tumorgenesis or hyperplastic growth of cells (Marshall, Cell, 64: 313-326 (1991); Weinberg, Science, 254:1138-1146 (1991)). Thus, changes in the expression levels of particular genes (*e.g.* oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening development. Often drugs are screened for the ability to interact with a major

target without regard to other effects the drugs have on cells. Often such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

The present inventors have examined tissue from normal prostate, BPH and BPH prostate tissue immediately adjacent to malignant prostate tissue to identify the global changes in gene expression in BPH. These changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, toxicity, drug efficacy and drug metabolism.

Assay Formats

The genes identified as being differentially expressed in BPH tissue or BPH cells (Tables 1-6) may be used in a variety of nucleic acid detection assays to detect or quantititate the expression level of a gene or multiple genes in a given sample. For example, traditional Northern blotting, nuclease protection, RT- PCR and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention, particularly when smaller numbers of genes are assayed. For instance, when fewer than 50 genes are assayed, RT-PCR techniques can be used to prepare high-throughput assays. However, methods and assays of the invention are most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

Any hybridization assay format may be used, including solution-based and solid support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, silicon or glass based beads or chips, etc. Such supports and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used.

A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or

400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of about a square centimeter.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any technique known in the art (see for example, Lockhart *et al.*, Nat. Biotechnol. (1996) 14, 1675-1680; McGall *et al.*, *Proc. Nat. Acad. Sci. USA* (1996) 93, 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 1-6 . For instance, such arrays may contain oligonucleotides that are complementary or hybridize to at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70 or more of the genes described herein.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not. The genes may be amplified or not. The cloning itself does not appear to bias the representation of genes within a population. However, it may be preferable to use polyA+ RNA as a source, as it can be used with less processing steps.

The sequences and related information of the genes described herein are available in the public databases. Tables 1-6 provide the Accession numbers and name for each of the sequences. Each Accession Number corresponds to a sequence in the attached sequence listing. The sequences and related information of the genes listed in the Tables according to their GenBank identifiers are expressly incorporated herein as of the filing date of this application, as are sequences in the databases related to those herein described, such as fragments, variant sequences, etc. (see: www.ncbi.nlm.gov).

Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for interrogating the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-6 refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at

the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, *etc.*). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (*e.g.* probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack probes.

The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular DNA or RNA).

Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 different nucleic acid hybridizations.

As used herein a "probe" is defined as a nucleic acid molecule, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical

bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5oC lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (*e.g.* nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Probe design

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes could be oligonucleotides that range from about 5 to about 500 or 5 to about 45 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect (the genes of Tables 1-6).

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes fall into three categories referred to herein as 1) normalization controls; 2) expression level controls; and 3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*, fluorescence

intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to an actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls or mismatch probes may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For

example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 *of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes*, Part I Theory and Nucleic Acid Preparation, P. Tijssen, Ed., Elsevier, N.Y. (1993). Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised in vitro, such as cell lines and tissue culture cells. Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes. Frequently, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to prostate tissue, urine, sputum, blood, blood-cells (*e.g.*, white cells or peripheral blood leukocytes (PBL), tissue or fine needle biopsy samples, peritoneal fluid, and pleural fluid, or cells therefrom.

Forming High Density Arrays.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling. See Pirrung *et al.*, U.S. Patent No. 5,143, 854.

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithogaphic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in WO 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary.

Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency in this case in 6X SSPE-T at 37°C (0.005% Triton X-100) to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, I X SSPE-T at 37oC) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25 X SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, *etc.*).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO 99/32660.

Databases

The present invention includes relational databases containing sequence information, for instance for the genes of Tables 1-6, as well as gene expression information in various prostate tissue samples. Databases may also contain information associated with a given

sequence or tissue sample such as descriptive information about the gene associated with the sequence information, metabolic pathway information for the gene or descriptive information concerning the clinical status of the tissue sample, or the patient from which the sample was derived. Such information for the patient may include, but is not limited to sex, age, disease status, general health information, surgical or treatment status, PSA levels, as well as information concerning the patient's clinical symptoms. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases are widely available, for instance, see U.S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 1-6, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such has those available from Silicon Graphics. Client/server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least two of the genes in Tables 1-6, comprising the step of comparing the expression level of at least one gene in Tables 1-6 found or detected in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the hyperplastic state of a given tissue by comparing the level of expression of a gene or genes in Tables 1-6 from a sample to the expression levels found in normal prostate cells, BPH cells or tissue and/or malignant or cancerous prostate tissue. Such methods may also be used in the drug or agent screening assays as described below.

Selection of BPH-Associated Genes

BPH associated genes may be identified or selected by any available method, including subtractive hybridization protocols, differential display protocols and high-throughput hybridization formats, including oligonucleotide and cDNA microarray technologies.

Unprocessed or raw expression levels may be normalized, standardized and/or analyzed by any available computational method, including the expression level normalization, analysis and clustering methods herein described. The normalization method as described in Example 4 may be combined with any further analysis method, including any clustering methods available in the art.

Diagnostic Uses for the BPH Markers

As described above, the genes and gene expression information provided in Tables 1-6 may be used as diagnostic markers for the prediction or identification of the hyperplastic state of a prostate or other tissue. For instance, a prostate tissue or other patient sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-6 may be compared to the expression levels found in normal prostate tissue, BPH tissue or BPH tissue from a patient with metastatic or nonmetastatic prostate cancer. In some instances, patient PBLs may be used as the patient sample. The comparison of expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the BPH Markers for Monitoring Disease Progression

As described above, the genes and gene expression information provided in Tables 1-6 may also be used as markers for the monitoring of disease progression, such as the development of BPH. For instance, a prostate tissue or other patient sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-6 may be compared to the expression levels found in normal prostate tissue, BPH tissue or BPH tissue from a patient with metastatic or nonmetastatic prostate cancer. The

comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

The BPH markers of the invention may also be used to track or predict the progress or efficacy of a treatment regime in a patient. For instance, a patient's progress or response to a given drug may be monitored by creating a gene expression profile from a tissue or cell sample after treatment or administration of the drug. The gene expression profile may then be compared to a gene expression profile prepared from normal cells or tissue, for instance, normal prostate tissue. The gene expression profile may also be compared to a gene expression profile prepared from BPH or malignant prostate cells, or from tissue or cells from the same patient before treatment. The gene expression profile may be made from at least one gene, preferably more than one gene, and most preferably all or nearly all of the genes in Tables 1-6.

Use of the BPH Markers for Drug Screening

According to the present invention, the genes identified in Tables 1-6 can be used as markers to screen for potential therapeutic agents or compounds to treat BPH or prostate cancer. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or to down-regulate or counteract the transcription or expression of a marker or markers. Compounds that modulate the expression level of single gene and also compounds that modulate the expression level of multiple genes from levels associated with a specific disease state to a normal state can be screened by using the markers and profiles identified herein.

According to the present invention, one can also compare the specificity of drug's effects by looking at the number of markers which are differentially expressed after drug exposure and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

Assays to monitor the expression of a marker or markers as defined in Tables 1-6 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a

nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to at least 2 genes from Tables 1-6 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described in more detail above. In another format, the changes of mRNA expression level can be detected using QuantiGene technology (Warrior *et. al.* (2000) *J. Biomolecular Screening*, 5, 343-351). Specific probes used for QuantiGene can be designed and synthesized to one or more genes from Tables 1-6. Cells treated with compounds are lysed by lysis buffer. The amount of target mRNA can be detected as a luminescence intensity using target specific probes.

In another format, cell lines that contain reporter gene fusions between the open reading frame and/or 5'/3' regulatory regions of a gene in Tables 1-6 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.* (1990) *Anal. Biochem.* 188:245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 1-6. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd Ed. Cold Spring Harbor Laboratory Press, 1989).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically (see below). Cell and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Such cell lines may be, but are not required to be, prostate derived. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector)

construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag or some other detectable marker or tag. Such a process is well known in the art (see Maniatis).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample is then compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control is used to distinguish the effectiveness of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 1-6. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, *etc.* An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant GA. in: Meyers (ed.) Molecular Biology and Biotechnology (New York, VCH Publishers, 1995), pp. 659-664). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Cells used for Multi Gene Screening

Many kinds of cells such as primary cells and cell lines can be used for the drug screening methods of the invention. Cells or cell lines derived from prostatic tissues are preferred because the innate gene expression mechanisms of these cells often resemble those of prostatic tissues. Cells used for drug screening can be selected by assaying for the expression of one or more of the marker genes listed in Tables 1-6. The cells which differentially express one or more, or preferably nearly all of the marker genes listed in Tables 1-6 are preferred cells or cell lines for the methods of the invention (see Table 7).

Kits

The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to diagnose the disease state of a tissue or cell sample, to monitor the progression of prostate disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

The databases packaged with the kits are a compilation of expression patterns from human and laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-6). In particular, the database software and packaged information include the expression results of Tables 1-6 that can be used in the assays and methods as herein described. In another format, database access is provided to the purchaser or user through an electronic means, *e.g.*, via the Internet or by direct dial-in access.

The kits may used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

Databases and software designed for use with use with microarrays is discussed in Balaban *et al.*, U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed tables, collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee *et al.*, U.S. Patent No. 5,974,164, disclose a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the genes, chips, *etc.* of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1: Gene chip expression analysis

Human tissue was obtained from the transitional zone of the prostate (the junction between the ejaculatory duct and the prostatic urethra) in biopsy samples from normal individuals and from patients with BPH or prostate cancer. BPH was defined histologically in all samples. Normal tissue and asymptomatic BPH samples came from individuals who died of trauma and did not report symptoms. Because BPH is a disease associated with aging, two groups of normal individuals were identified, group 1, ages 20 or under, and group 2, ages 30-50. Patients having BPH with symptoms were defined as those with a need for frequent urination. In these patients, a radical prostatectomy had been performed. Prostate cancer patients provided age-matched tissue samples for symptomatic BPH patients, but were without symptoms and without cancer in the transitional zone under histological examination.

Microarray sample preparation was conducted with minor modifications, following the protocols set forth in the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500 μg per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded cDNA was generated from mRNA using the SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 μg/ml. From 2 μg of cDNA, cRNA was synthesized using Ambion's T7 MegaScript *in vitro* Transcription Kit.

To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. Following a 37°C incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol

(Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Tris-acetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C. Following the Affymetrix protocol, 55 µg of fragmented cRNA was hybridized on the Affymetrix Human 42K array set for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Data was analyzed using Affymetrix GeneChip version 3.0 and Expression Data Mining Tool (EDMT) software (version 1.0).

Differential expression of genes between the BPH and normal prostate samples were determined using the Affymetrix GeneChip human gene chip set by the following criteria: 1) For each gene, Affymetrix GeneChip average difference values were determined by standard Affymetrix EDMT software algorithms, which also made "Absent" (=not specifically detected as gene expression), "Present" (=detected) or "Marginal" (=not clearly Absent or Present) calls for each GeneChip element; 2) all AveDiff values which were less than +20 (positive 20) were raised to a floor of +20 so that fold change calculations could be made where values were not already greater than or equal to +20; 3) median levels of expression were compared between the normal control group and the BPH with symptoms disease group to obtain greater than or equal 2-fold up/down values; 4) The median value for the higher expressing group needed to be greater or equal to 200 average difference units in order to be considered for statistical significance; 5) Genes passing the criteria of #1-4 were analyzed for statistical significance using a two-tailed T test and deemed statistically significant if $p < 0.05$. Tables 1 and 2 list the genes and their levels of differential expression (compared to normal samples) in BPH tissue from patients with symptoms of BPH and in BPH tissue immediately adjacent to malignant prostate tissue isolated from male patients.

Example 2 : Expression profile analysis

Gene expression profiles between normal sample and BPH patient samples were determined by using the following samples: 10 normal; 7 BPH without symptoms; 8 BPH with cancer; and 8 BPH with symptoms. Gene expression profiles were prepared using the

42K Affymetrix Gene Chip set. The methods used were the same as described in Example 1 with the exception of the criteria to select the marker genes.

The criteria used in this study were as follows; 1) For each gene, Affymetrix GeneChip average difference values were determined by standard Affymetrix EDMT software algorithms, which also made "Absent" (=not specifically detected as gene expression), "Present" (=detected) or "Marginal" (=not clearly Absent or Present) calls for each GeneChip element; 2) all AveDiff values which were less than +20 (positive 20) were raised to a floor of +20 so that fold change calculations could be made where values were not already greater than or equal to +20; 3) mean levels of expression were compared between the normal control group and the BPH with symptoms disease group; 4) genes were arranged by the fold change starting with the largest one (Fold change calculation was determined by using logarithmic values in Example 2); and 5) the top 200 up-regulated genes and bottom 200 down-regulated genes were selected. The genes identified in this study are listed in Tables 3 (normal vs. BPH with symptoms, up regulated) and 4 (normal vs. BPH with symptoms, down regulated, values are negative fold-change from normal).

Example 3 : Selection of Cell lines used for Multi Gene Screening

A number of cultured cell lines were tested to determine the similarity in gene expression profiles to BPH tissue. Cells were cultured in 6-well plates using the appropriate medium for each cell line. After reaching 90% confluency, cells were lysed with Trizol (GiboBRL) and total RNA was extracted. mRNA was then isolated, cDNA and cRNA was synthesized, and gene expression levels were determined by the Affymetrix Human 42K Gene Chip set as described in more detail above.

The gene expression profiles were compared with those of prostatic tissue samples. A panel of 61 genes whose expression levels were up-regulated in BPH with symptoms compared with normal samples and with small variation among samples (within BPH samples and within normal samples) were assayed. The group of genes whose signal intensity was more than 100 in each cell line is summarized in Table 1. A panel of 43 genes whose expression levels were down-regulated in BPH patient with small variation among samples was also assayed. The group of genes whose signal intensity in Affymetrix Gene Chip was "Present call" is also included in Table 1. Similarly, genes whose expression level

is up- or down-regulated in patients with BPH and cancer, compared to normal controls, are listed in Table 2.

Forty-eight to 58% of genes applied for this analysis were expressed in the cell lines of Table 7. These results indicate that cell lines, BRF-55T (Biological Research Faculty & Facility Inc.), PZ-HPV7 (ATCC; CRL-2221) , BPH-1 (S.W. Hayward *et al.*, *In Vitro Cell Dev. Biol.* 31A, 14-24, 1995) and LNCaP (ATCC; CRL-1740) can be used as a BPH – like cell population to screen for compounds which are capable of modulating gene expression profiles from the disease state to a normal state using the genes of Tables 1-6. In particular, BRF-55T is a useful cell line for screening in the assays of the invention, because 58% genes of the assayed genes were differentially expressed in BRF-55T as compared to BPH with symptoms tissue.

Example 4 : Cluster analysis of up- or down-regulated genes in BPH

Cluster analysis of the expression results from a large number of genes is often problematic due to variations in the standardization of the gene expression data. To compensate for these variations, a subset of differentially expressed genes was selected by a modified analysis procedure.

In a first step, a gene list comparing normal vs. disease samples was generated by two kinds of comparisons. First, genes were selected that displayed a greater than or equal to mean 2-fold up or down regulation using average difference expression values and with $p<0.05$. Second, genes were selected by ANOVA comparing the normal group of samples with the disease group and with a t value of >3 in the up or down direction. These lists were then combined to create an expression profile characteristic of normal controls and one characteristic of disease in which specific genes are found to be up or down regulated in disease when compared with normal controls.

In preparation for clustering analysis to identify subgroups of genes that show statistically similar expression patterns, average difference values for the selected genes were normalized across all samples (normal and disease combined) using the following formula:

Normalization data = (X - Xmean)/Sx

Where Sx is variance (:STD)

This converts the mean expression value for each gene to 0 and the high and low values to 1 and –1, respectively. Thus, genes with high absolute expression values when compared with genes with low absolute expression values would not skew the comparisons when clustering algorithms are applied.

The measurement of the cluster space distance was determined by using the correlation coefficient (1-r) method and clustering was performed using Ward's method (Ward,J.H. (1963) *Journal of American Statistical Association*, 58. 236.)

The clustering was validated by observing whether multiple elements representing the same genes showing the same direction of expression change (*i.e.*, either up or down) tend to cluster together. To test this standardization and clustering protocol, the expression levels for genes that are represented by more than one element on the 42K gene chip set were analyzed to determine whether the multiple elements for a single gene could be clustered together. For example, tryptase, also known as alpha tryptase or beta (tryptase II) is represented by two separate elements on the 42K human gene chip. This gene is registered with 2 different element names 41268 (5), M33493_s_at (code name, Up-170) and 26389 (3), rc_AA131322_s_at (code name, Up-010).

It was found that the best analysis means for decreasing measurement errors between these two elements is by the Ward method as it gave the most consistent results when compared to other clustering methods. These analysis methods may be incorporated into software or computer readable storage media for storing a computer programmer software.

Example 5 : Selection of 60 Marker Genes

A panel of 60 representative marker genes (listed in Table 5) out of 400 marker genes listed in Tables 3 and 4 can be used in the assays and methods of the invention. The 60 marker genes were selected based on following criteria: (1) expression level is changed greatly in BPH patient samples compared with normal samples; (2) variation of expression levels within BPH samples and within normal samples is small; and (3) expression levels resembling BPH with symptoms are detected in cell line BRF-55T.

Example 6: Gene Expression Analysis of Select Genes

The expression levels of three genes from Tables 1-5 (the genes encoding cellular retinol binding protein, S100 calcium binding protein and PSMA) were assayed in various tissues and prostate samples by PCR as described in Example 7 (see Figures 1-6). Each sample was assayed for the level of GAPDH and mRNA corresponding to cellular retinol binding protein, S100 calcium binding protein or PSMA. As seen in Figures 1-6, these three genes are differentially regulated or expressed in BPH tissue from patients with or without symptoms and from BPH tissue from patients with prostate cancer (compared to normal prostate tissue). All three genes are therefore useful markers in the assays of the invention, such as the assays to measure the effect of an agent on BPH or the assays to detect or diagnose the occurrence or progression of BPH.

Example 7: Drug Screening Assays

The expression profiles for normal controls and disease samples described above can be used to identify compound hits from a compound library. A hit may be, but is not necessarily, defined as one of three kinds of results:

1) The expression of an individual gene is changed in the direction of normal (*i.e.*, if up in disease, then down=hit, if down in disease, then up=hit). The stronger the modulation of an individual gene to a normal phenotype, the stronger the hit status for the compound against that gene.

2) The expression of genes that subcluster together is evaluated for an overall pattern of modulation to a normal expression profile. The more genes in a subcluster that are modulated to a normal phenotype, the stronger the hit status for the compound against that subcluster. A subcluster may represent common or interacting cellular pathways.

3) The overall expression profile of all of the genes being screened is evaluated for modulation to normal. The more genes that are modulated to a normal phenotype, the stronger the hit status for the compound against the entire gene set.

As described above, if a compound modulates the gene expression pattern of the screening system cells more towards any disease phenotype, then it can be used as a molecular probe to find binding proteins and/or define disease-associated cellular pathways.

As an example, candidate agents and compounds are screened for their ability to modulate the expression levels of cellular retinol binding protein, S100 calcium binding

protein and PSMA by exposing a prostate cell line or cell line from BPH tissue to the agent and assaying the expression levels of these genes by real time PCR. Real time PCR detection is accomplished by the use of the ABI PRISM 7700 Sequence Detection System. The 7700 measures the fluorescence intensity of the sample each cycle and is able to detect the presence of specific amplicons within the PCR reaction. Each sample is assayed for the level of GAPDH and mRNA corresponding to cellular retinol binding protein, S100 calcium binding protein and PSMA. GAPDH detection is performed using Perkin Elmer part#402869 according to the manufacturer's directions. Primers were designed for the three genes by using Primer Express, a program developed by PE to efficiently find primers and probes for specific sequences ((1) N91971 - FAM PROBE Forward: 5'- CAT ggC TTT gTT TTA AgA AAA ggA A -3'; Reverse: 5'- AgC CAC CCC CAg gCA T -3'; Probe: 5'-FAM - AgT gAC AAA gCC AAg AgA CAg ACT CTg CTA ACA - TAMRA-3'; (2) X65614 – SYBR; Forward: 5'- AAA gAC AAg gAT gCC gTg gAT -3'; Reverse 5'-AgC CAC gAA CAC gAT gAA CTC-3'; (3) M99487-SYB; Forward 5'-Tgg CTC AgC ACC ACC Aga T-3'; Reverse: 5'-TTC Cag TAA AgC Cag gTC CAA-3')

These primers are used in conjunction with SYBR green (Molecular Probes), a nonspecific double stranded DNA dye, to measure the expression level mRNA corresponding to the genes, which is normalized to the GAPDH level in each sample.

Normalized expression levels from cells exposed to the agent are then compared to the normalized expression levels in control cells. Agents that modulate the expression of one or more the genes may be further tested as drug candidates in appropriate BPH *in vitro* or *in vivo* models.

Example 8: Comparative assays

The expression of a panel of marker genes was compared, in the same subjects as disclosed in Example 2, in a pairwise fashion between the BPH patients with (BPHWS) or without (BPHNoS) symptoms versus normal (Normal) controls and asymptomatic BPH patients with cancer (Cancer). In every case, the tissue was excised from the junction between the ejaculatory duct and the prostatic urethra in the transition zone of the prostate. In particular, BPH tissue from patients with early stage prostate cancer was carefully excised away from the cancer lesion macroscopically, and their histological diagnosis was confirmed microscopically.

Pairwise comparisons between the subject groups were subjected to an Analysis of Variance (ANOVA) model. P-values corresponding to each of six possible pairwise comparisons among the four sample groups were then determined for each gene. Table 6 depicts Affymetrix fragments, along with their GenBank accession number, which have $p<0.001$ for two or more of the pairwise comparisons.

A Principal Component Analysis (PCA) was performed to show that this gene set serves as a basis to discriminate among the various groups of samples. The samples are plotted using the scores for the first three principal components. Each of the four sample groups can be clearly distinguished from one another in this analysis (Figure 7A). Component 1 (36% of the variability) discriminates between Normal and asymptomatic BPH versus BPH cancer and symptomatic BPH. Component 2 (10% of the variability) distinguishes Normal from asymptomatic BPH, and Component 3 (8% of the variability) distinguishes BPH cancer from symptomatic BPH.

Figure 7B shows a two-dimensional representation of the PCA, with Component 1 plotted against Components 2 + 3. Each of the four sample groups is clustered in a different quadrant of this figure. Within each sample group, there does not appear to be any age-related clustering of samples. Further, since there is an overlap of ages between the samples groups, it does not appear that age was a confounding factor for the analysis based on this gene set. Because BPH is perceived as a natural consequence of aging, two subgroups of normal individuals were initially identified. A 'younger' set included individuals ranging in age from 13-20 years while the 'older' set ranged from 31-51 years. However, because the two subsets appeared to be indistinguishable at the molecular level, they were grouped together and in all subsequent analysis referred to as 'Normal' group.

Another finding was that the intra-group variability (*i.e.*, the tightness of clustering) differed between the four groups (Figure 7A). Normal patients exhibited the least intra-group variability, followed by asymptomatic BPH and symptomatic BPH with BPH cancer patients exhibiting the most patient-to-patient variability. On the other hand, with regard to the inter-group variation, the asymptomatic BPH group appeared to be more similar to the normal group than to symptomatic BPH (Figure 7B).

Asymptomatic BPH samples were obtained from individuals that died from other causes and had no records of being treated for BPH but had histological evidence for BPH when examined retrospectively. Since asymptomatic samples clearly exhibit the BPH phenotype at the microscopic level, one would expect the two BPH groups to exhibit more

similarity than disparity. Similarly, that the BPH cancer group is distinct from asymptomatic BPH but is more similar to the symptomatic BPH group (Figure 7B). Since transition zone tissue from patients with prostate cancer with no clinical symptoms of BPH was analyzed from these patients, this group of patients would be expected to appear similar to normal or asymptomatic BPH. The fact that the BPH cancer group can be distinguished from every other group is also an unexpected finding. Subsequent to this PCA, additional samples were studied to extend these findings. These included two normals and three symptomatic BPH patients. Using the same set of genes, a PCA was performed with these additional samples. In Figure 7C, the two new normal (Norm) samples group with the previous normal samples and the three new symptomatic BPH (BPH) samples group with the other symptomatic BPH samples.

Example 9: Diagnostic assays

The expression profiles or one or more of the individual genes of Tables 1-6 are used as molecular or diagnostic markers to evaluate the disease status of a patient sample. In one embodiment, a patient prostate tissue sample is processed as described herein to produce total cellular or mRNA. The RNA is hybridized to a chip continuing probes that specifically hybridize to one or more, or two or more of the genes in Tables 1-6. The overall expression profile generated, or the expression levels of individual genes are then compared to the profiles as described in Tables 1-6 to determine the disease or hyperplastic state of the patient sample.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, applications, GenBank Accession numbers and publications referred to in this application are herein incorporated by reference in their entirety.

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_AA463726_s_at	386	AA463726	JM27 proteinXp11.23	14.9	0.018598344
	RC_AA057195_at	47	AA057195	Homo sapiens mRNA; cDNA DKFZp586M121 (from clone DKFZp586M121)	14.0	0.029325045
	V01512_rna1_at	993	V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	13.1	0.001027561
	RC_AA427622_s_at	311	AA427622	collagen, type XIII, alpha 110q22	11.6	0.00074954
	RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	11.4	0.000631487
	RC_AA465491_at	391	AA465491	Mad4 homolog4p16.3	11.4	0.031024189
	RC_AA620825_at	454	AA620825	ESTs	11.3	0.010915901
	RC_R93908_at	865	R93908	ESTs	11.3	0.019994337
	RC_AA461300_at	381	AA461300	ESTs	11.0	0.007061759
	N40141_at	743	N40141	JM27 proteinXp11.23	10.9	0.013756347
	RC_R25410_at	814	R25410	ESTs	7.7	0.01851753
	L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	7.4	0.041523744
	RC_AA279760_at	193	AA279760	ESTs	7.0	0.024411468
	RC_T90889_at	927	T90889	ESTs	6.5	0.015666863
	U62015_at	978	U62015	insulin-like growth factor binding protein 101p22-p31	6.0	0.002843661
	RC_AA188981_at	112	AA188981	highly expressed in cancer, rich in leucine heptad repeats	5.9	0.002280479
	D83018_at	513	D83018	nel (chicken)-like 212q13.11-q13.12	5.6	0.000570952
	RC_H64493_f_at	590	H64493	immunoglobulin gamma 3 (Gm marker)14q32.33	5.6	0.01109802
	X52541_at	1064	X52541	early growth response 15q31.1	5.2	0.002428259
	M57466_s_at	690	M57466	major histocompatibility complex, class II, DP beta 16p21.3	5.1	0.002137399
	J03507_at	621	J03507	complement component 75p13	4.9	1.36616E-05
	RC_N30198_at	733	N30198	ESTs	4.8	0.003366461
	RC_T78398_at	913	T78398	EST	4.8	0.033293747
	RC_H17550_at	559	H17550	ESTs	4.7	0.047828622
	RC_T67053_f_at	909	T67053	immumoglobulin lambda gene cluster22q11.1-q11.2	4.5	0.045107075
	RC_AA598982_s_at	429	AA598982	trophininXp11.22-p11.21	4.3	0.000902336
	RC_AA256268_at	175	AA256268	ESTs	4.2	0.001506239
	HG3543-HT3739_at	675	M29645	insulin-like growth factor 2 (somatomedin A)11p15.5	4.1	0.017253126
	RC_N91971_f_at	791	N91971	retinol-binding protein 1, cellular3q23	4.1	0.02528773
	RC_AA479286_at	403	AA479286	ESTs	4.0	0.028009544
	M62831_at	695	M62831	immediate early protein19	4.0	0.000484086
	RC_F02992_at	526	F02992	ESTs, Weakly similar to unknown [M.musculus]	3.9	0.031845412
	RC_H86112_f_at	600	H86112	KIAA0471 gene product1q24-q25	3.8	0.004155259
	RC_AA436616_at	335	AA436616	ESTs	3.8	0.017156387
	RC_T62857_at	903	T62857	ESTs	3.7	0.000301735
	RC_AA281345_f_at	201	AA281345	immediate early protein19	3.6	0.001679723
	U21128_at	953	U21128	lumican12q21.3-q22	3.6	2.19529E-05
	U30521_at	960	U30521	P311 protein	3.6	0.001150397
	RC_N58172_at	757	N58172	ESTs	3.5	0.043092144
	RC_T03229_f_at	874	T03229	EST	3.5	0.031101935

Doc#: 1669617.1

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	X06700_s_at	1049	X06700	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)2q31	3.5	0.008472599
	RC_Z39904_at	1111	Z39904	Homo sapiens clone 23555 mRNA sequence	3.4	0.002949046
	RC_T23622_at	886	T23622	ESTs	3.4	0.002174281
	J00231_f_at	617	J00231	immunoglobulin gamma 3 (Gm marker)14q32.33	3.4	0.009322568
	RC_AA028092_s_at	17	AA028092	transcription factor 216pter-qter	3.4	3.13963E-06
	RC_AA252528_at	170	AA252528	ESTs	3.4	0.000225707
	L33799_at	645	L33799	procollagen C-endopeptidase enhancer7q22	3.3	0.018469201
	RC_F09748_s_at	537	F09748	Homo sapiens mRNA; cDNA DKFZp586K1220 (from clone DKFZp586K1220)	3.2	0.02728166
	RC_T64223_s_at	907	T64223	carboxypeptidase A3 (mast cell)3q21 q25	3.2	0.027915742
	RC_AA402903_f_at	263	AA402903	immunoglobulin gamma 3 (Gm marker)14q32.33	3.2	0.044721116
	RC_F13763_at	542	F13763	ESTs	3.1	0.000503701
	RC_AA488432_at	412	AA488432	phosphoserine phosphatase7p21-p15	3.1	0.020997503
	RC_AA486072_i_at	410	AA486072	small inducible cytokine A5 (RANTES)17q11.2-q12	3.1	0.025877597
	RC_N22006_s_at	719	N22006	EST	3.1	0.00148561
	RC_AA257093_r_at	178	AA257093	T-cell receptor, beta cluster7q35	3.1	1.71945E-07
	RC_AA609943_at	449	AA609943	ESTs	3.0	0.029360518
	RC_T23490_s_at	885	T23490	ESTs	3.0	0.008741411
	D13628_at	476	D13628	angiopoietin 18q22.3-q23	2.9	0.006228419
	M73720_at	702	M73720	carboxypeptidase A3 (mast cell)3q21 q25	2.9	0.006585391
	Z74616_s_at	1123	Z74616	collagen, type I, alpha 27q22.1	2.8	0.008750622
	AA082546_at	54	AA082546	ESTs	2.8	0.019771126
	RC_AA284920_at	213	AA284920	ESTs	2.7	0.019738239
	RC_AA599365_at	434	AA599365	decorin12q23	2.7	0.001295936
	X57025_at	1066	X57025	insulin-like growth factor 1 (somatomedin C)12q22-q23	2.7	0.022341194
	X51345_at	1062	X51345	jun B proto-oncogene19p13.2	2.7	0.036487159
	RC_N67876_s_at	773	N67876	insulin-like growth factor 1 (somatomedin C)12q22-q23	2.7	0.035216134
	RC_AA609504_at	444	AA609504	KIAA0405 gene product	2.7	0.020881055
	RC_N69207_at	776	N69207	ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]	2.6	0.041315387
	M87789_s_at	704	M87789	immunoglobulin gamma 3 (Gm marker)14q32.33	2.6	0.038916248
	HG3510-HT3704_at	1055	X12795	nuclear receptor subfamily 2, group F, member 15q14	2.6	0.016151338
	RC_T64211_at	906	T64211	ESTs, Weakly similar to pancortin-1 [M.musculus]	2.6	0.006233291
	U90552_s_at	988	U90552	butyrophilin, subfamily 3, member A16p23	2.6	0.004564282
	M34516_r_at	684	M34516	immunoglobulin lambda-like polypeptide 322q11.2	2.6	0.049767038

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_T23468_at	884	T23468	ESTs	2.5	0.00250737
	RC_AA173223_at	108	AA173223	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	2.5	0.007080285
	RC_T49061_at	894	T49061	ESTs	2.5	0.039642391
	RC_AA234095_at	144	AA234095	ESTs	2.5	0.003152859
	RC_F01920_s_at	520	F01920	pre-B-cell leukemia transcription factor 39q33-q34	2.5	0.002088945
	RC_N91461_at	789	N91461	ESTs	2.4	0.01015467
	RC_N67575_s_at	771	N67575	osteoglycin (osteoinductive factor)	2.4	0.004044061
	RC_AA151210_at	89	AA151210	ESTs	2.4	0.011476541
	AA156897_s_at	97	AA156897	Homo sapiens mRNA; cDNA DKFZp564I1922 (from clone DKFZp564I1922)	2.4	0.033974981
	W73859_at	1028	W73859	transcription factor 216pter-qter	2.4	0.024640626
	RC_H68097_at	592	H68097	EST	2.4	0.04870874
	RC_AA436618_at	336	AA436618	ESTs	2.4	0.02483165
	M33493_s_at	680	M33493	tryptase, beta (tryptase II)16p13.3	2.4	0.02689938
	AB002340_at	461	AB002340	KIAA0342 gene product	2.3	0.000748796
	RC_AA446661_at	347	AA446661	ESTs	2.3	0.011980248
	RC_AA084138_at	55	AA084138	ESTs	2.3	1.16025E-05
	RC_N59866_at	761	N59866	ESTs, Weakly similar to putative p150 [H.sapiens]	2.3	0.002042263
	RC_R42424_at	832	R42424	ESTs	2.3	0.003173074
	RC_N39415_at	742	N39415	osteoglycin (osteoinductive factor)	2.3	0.001310764
	J03464_s_at	620	J03464	collagen, type I, alpha 27q22.1	2.3	0.006791534
	RC_AA205376_at	121	AA205376	KIAA0471 gene product1q24-q25	2.3	0.023123837
	RC_H95960_at	606	H95960	secreted protein, acidic, cysteine-rich (osteonectin)5q31.3-q32	2.3	0.008509182
	D28137_at	484	D28137	bone marrow stromal cell antigen 219p13.2	2.3	0.031127266
	RC_N79778_at	784	N79778	extracellular matrix protein 2, female organ and adipocyte specific9q22.3	2.3	0.045073744
	RC_N98485_s_at	800	N98485	forkhead (Drosophila)-like 66p25.3	2.3	0.033372862
	M98539_at	715	M98539	prostaglandin D2 synthase (21kD, brain)9q34.2-q34.3	2.2	0.005442674
	RC_AA205724_at	123	AA205724	ESTs	2.2	0.006183612
	U85625_at	986	U85625	Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.	2.2	0.001245066
	RC_R37588_s_at	821	R37588	RAB2, member RAS oncogene family-like6p21.3	2.2	0.00219386
	RC_AA046426_at	35	AA046426	Cdc42 effector protein 3	2.2	0.005788723
	RC_AA256294_at	176	AA256294	ESTs	2.2	0.002425605
	RC_AA599120_at	431	AA599120	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	2.2	0.042979241
	RC_W60186_at	1018	W60186	ESTs	2.2	0.028494835
	RC_AA599216_at	432	AA599216	collapsin response mediator protein 14p16.1-p15	2.2	0.040523744
	RC_AA450324_at	360	AA450324	ESTs	2.1	0.009094567
	M31994_at	678	M31994	Homo sapiens aldehyde dehydrogenase (ALDH1) gene	2.1	0.001561218

10452030.060501

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_AA402930_at	264	AA402930	ESTs	2.1	0.000114627
	M91029_cds2_at	706	M91029	Human AMP deaminase isoform L (AMPD2) mRNA, exons 6-18, partial cds	2.1	0.02494373
	RC_AA450114_at	358	AA450114	ESTs, Weakly similar to 17beta-hydroxysteroid dehydrogenase [H.sapiens]	2.1	4.87556E-06
	D62584_at	501	D62584	osteoglycin (osteoinductive factor)	2.1	0.000157116
	RC_AA621634_at	457	AA621634	ESTs	2.1	0.02297009
	RC_AA312946_s_at	228	AA312946	ESTs	2.1	3.51075E-05
	X07438_s_at	1054	X07438	Human DNA for cellular retinol binding protein (CRBP)	2.1	0.039015947
	RC_N53447_at	751	N53447	integral membrane protein 2CXq21.1-21.2	2.1	0.009032297
	RC_AA281591_at	202	AA281591	Homo sapiens mRNA; cDNA DKFZp586B211 (from clone DKFZp586B211)	2.0	0.016660714
	RC_R71395_at	854	R71395	ESTs, Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	2.0	0.046231847
	RC_T53590_s_at	899	T53590	cytochrome P450, subfamily XIA (cholesterol side chain cleavage)15q23-q24	2.0	0.00282074
	RC_AA293489_at	224	AA293489	KIAA0638 protein	2.0	0.006966532
	RC_AA447707_s_at	351	AA447707	KIAA1055 protein	2.0	0.001248537
	RC_AA235618_f_at	149	AA235618	ESTs	2.0	0.012481746
	RC_N68350_at	775	N68350	ESTs	2.0	0.035156598
	RC_H81379_s_at	596	H81379	ESTs, Moderately similar to KIAA0438 [H.sapiens]	2.0	0.01148429
	RC_D51060_s_at	495	D51060	Jun activation domain binding protein1p32-p31	2.0	0.016668951
	U72649_at	983	U72649	B-cell translocation gene 2 (pheochromacytoma cell-3)1q32	2.0	0.020660388
	RC_AA287389_at	216	AA287389	ESTs	2.0	0.002741873
	RC_AA621367_at	456	AA621367	ESTs	2.0	0.004871903
	J03040_at	619	J03040	secreted protein, acidic, cysteine-rich (osteonectin)5q31.3-q32	2.0	0.006303994
	RC_AA291676_s_at	219	AA291676	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)5q23-q31	2.0	0.027480479
	RC_N63536_at	763	N63536	ESTs	2.0	0.000634305
	RC_AA411952_at	282	AA411952	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 33q25	2.0	0.011858934
	RC_AA252802_s_at	171	AA252802	Human mRNA for TI-227H	2.0	0.041027635
	RC_AA382275_at	244	AA382275	ESTs	2.0	0.00087437
	AA093923_at	63	AA093923	tissue inhibitor of metalloproteinase 217q25	2.0	0.046200886
	M11313_s_at	654	M11313	alpha-2-macroglobulin12p13.3-p12.3	2.0	0.013660595
	RC_AA398280_at	248	AA398280	ESTs	2.0	0.044320644
	RC_N51529_at	747	N51529	ESTs	2.0	0.006276979
	H49440_at	578	H49440	nudix (nucleoside diphosphate linked moiety X)-type motif 36p21.2	2.0	0.013879331

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_T33263_s_at	890	T33263	KIAA0320 protein	2.0	0.009994615
	RC_T89160_r_at	921	T89160	ESTs	2.0	0.005289266
	RC_W56792_at	1016	W56792	ESTs, Weakly similar to serine/threonine protein kinase TAO1 [R.norvegicus]	2.0	0.026130523
	RC_R60056_at	849	R60056	ESTs, Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	2.0	0.001585076
Down-regulated	RC_AA398908_at	251	AA398908	Human Chromosome 16 BAC clone CIT987SK-A-61E3	-21.7	0.007918174
	RC_AA460914_at	380	AA460914	ESTs	-15.8	0.013659536
	RC_T40895_at	892	T40895	ESTs	-12.6	0.002430219
	RC_R71792_s_at	855	R71792	ESTs, Moderately similar to FAT-SPECIFIC PROTEIN FSP27 [M.musculus]	-9.8	0.01438632
	RC_N80129_i_at	785	N80129	metallothionein 1L16q13	-8.7	0.002816872
	X66141_at	1078	X66141	myosin, light polypeptide 2, regulatory, cardiac, slow12q23-q24.3	-8.0	0.03928942
	AA234634_f_at	145	AA234634	CCAAT/enhancer binding protein (C/EBP), delta8p11.2-p11.1	-7.4	0.000589696
	U78294_at	985	U78294	arachidonate 15-lipoxygenase, second type	-6.8	0.017271608
	RC_AA457566_at	375	AA457566	ESTs	-6.6	0.029644622
	X93036_at	1093	X93036	phospholemman-like, expressed in breast tumors, 8kD	-6.2	0.011323909
	X57129_at	1067	X57129	H1 histone family, member 26p21.3	-6.1	0.004161922
	HG1067-HT1067_r_at	671	M22406	Human intestinal mucin mRNA, partial cds, clone SMUC 42	-5.8	0.007202185
	X65614_at	1076	X65614	S100 calcium-binding protein P4p16	-5.8	0.006892572
	RC_AA609006_at	440	AA609006	ESTs	-5.7	0.015701354
	J03910_rna1_at	622	J03910	metallothionein 1G16q13	-5.7	0.003506953
	RC_H94471_at	604	H94471	occludin5q13.1	-5.6	0.025014274
	AB000584_at	459	AB000584	prostate differentiation factor	-5.4	0.003235425
	RC_W88568_at	1035	W88568	glycogenin 2Xp22.3	-5.1	0.048573115
	V00594_at	992	V00594	metallothionein 2A16q13	-5.0	0.000721258
	RC_T73433_s_at	912	T73433	angiotensinogen1q41-qter	-4.9	0.012700144
	RC_N94303_at	797	N94303	ESTs	-4.5	4.88059E-05
	RC_AA419011_at	296	AA419011	Homo sapiens mRNA; cDNA DKFZp586D0823 (from clone DKFZp586D0823)	-4.1	0.013801595
	RC_N32748_at	736	N32748	ESTs	-4.1	0.018749207
	RC_AA053424_at	40	AA053424	ESTs, Weakly similar to mucin Muc3 [R.norvegicus]	-4.0	0.001235197
	RC_AA599331_at	433	AA599331	ESTs	-4.0	0.005480655
	M99487_at	716	M99487	folate hydrolase (prostate-specific membrane antigen) 111p11.2	-3.9	0.013268152
	RC_F02245_at	522	F02245	monoamine oxidase AXp11.4-p11.3	-3.8	0.002950391
	X76717_at	1087	X76717	metallothionein 1L16q13	-3.7	0.000868707

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	X64177_f_at	1075	X64177	metallothionein 1H16q13	-3.7	0.002089771
	RC_AA599522_r_at	437	AA599522	squamous cell carcinoma antigen recognised by T cells	-3.6	0.012643918
	L77701_at	651	L77701	human homolog of yeast mitochondrial copper recruitment gene	-3.6	0.003341007
	RC_D11824_at	474	D11824	ESTs, Moderately similar to weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [C.elegans]	-3.6	0.000803294
	RC_AA410311_at	275	AA410311	ESTs	-3.5	0.001234064
	RC_AA457235_at	373	AA457235	ESTs	-3.5	0.012177965
	RC_N93798_at	796	N93798	protein tyrosine phosphatase type IVA, member 3	-3.5	0.007340453
	RC_AA416762_s_at	291	AA416762	nuclear receptor subfamily 1, group H, member 219q13.3-19q13.3	-3.5	0.010404304
	RC_F03969_at	528	F03969	ESTs, Weakly similar to tumorous imaginal discs protein Tid56 homolog [H.sapiens]	-3.5	0.011826812
	RC_AA045487_at	31	AA045487	ESTs	-3.4	0.025187615
	RC_Z38744_at	1108	Z38744	putative gene product13	-3.4	2.30674E-05
	RC_N92502_s_at	794	N92502	ESTs, Moderately similar to HERV-E integrase [H.sapiens]	-3.4	0.02301359
	RC_R91484_at	863	R91484	ESTs	-3.4	8.2306E-05
	RC_AA165313_at	104	AA165313	ESTs	-3.3	0.028364404
	RC_AA182030_at	110	AA182030	ESTs	-3.3	0.019770486
	RC_T94447_s_at	928	T94447	ESTs, Moderately similar to (defline not available 4335935) [M.musculus]	-3.3	0.001427294
	RC_W20486_f_at	995	W20486	ESTs	-3.3	0.002892697
	RC_R16983_at	811	R16983	ESTs	-3.2	0.000912559
	RC_AA504805_s_at	424	AA504805	interferon stimulated gene (20kD)15q26	-3.2	0.003905701
	RC_T90190_s_at	925	T90190	H1 histone family, member 26p21.3	-3.2	0.020618793
	RC_AA135870_at	79	AA135870	ESTs	-3.1	0.04609197
	RC_H99035_at	612	H99035	ESTs	-3.1	0.000191451
	RC_R28370_at	815	R28370	ESTs	-3.1	0.024606319
	RC_T40995_f_at	893	T40995	alcohol dehydrogenase 3 (class I), gamma polypeptide4q21-q23	-3.1	0.024064044
	MIP1-B_at	1124	M35590	karyopherin (importin) beta 2	-3.1	0.005882353
	RC_AA447522_at	349	AA447522	ESTs, Highly similar to differentially expressed in Fanconi anemia [H.sapiens]	-3.1	0.003518059
	RC_AA461453_at	382	AA461453	ESTs, Moderately similar to Cab45a [M.musculus]	-3.0	0.021949087
	AA429539_f_at	318	AA429539	ESTs	-3.0	0.017623102
	RC_AA476944_at	394	AA476944	ESTs	-3.0	0.019974254
	RC_N80129_f_at	785	N80129	metallothionein 1L16q13	-3.0	0.000219038
	RC_N26904_at	731	N26904	ESTs, Weakly similar to FK506/rapamycin-binding protein FKBP13 precursor [H.sapiens]	-2.9	0.006305062
	RC_AA505136_at	426	AA505136	ESTs	-2.9	0.005400284
	AA455001_s_at	368	AA455001	ESTs	-2.9	2.1534E-05
	RC_W70131_at	1024	W70131	ESTs	-2.9	0.005764635

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms 1669617.1

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_AA043349_at	27	AA043349	ESTs	-2.9	0.016983419
	U02020_at	936	U02020	pre-B-cell colony-enhancing factor	-2.9	0.003324497
	U52969_at	970	U52969	Purkinje cell protein 421q22.2-q22.3	-2.8	0.00078638
	RC_H22453_at	564	H22453	ESTs	-2.8	0.000410695
	RC_N22620_at	722	N22620	ESTs	-2.8	0.005507089
	RC_N64683_at	764	N64683	ESTs	-2.8	0.00378977
	RC_N24761_at	725	N24761	ESTs	-2.8	0.004837185
	RC_AA464728_s_at	388	AA464728	ESTs	-2.8	0.004669897
	RC_H83380_at	598	H83380	ESTs	-2.7	0.016543793
	M30894_at	676	M30894	T-cell receptor, gamma cluster7p15-p14	-2.7	0.034153167
	RC_H81070_f_at	595	H81070	Human metallothionein (MT)I-F gene	-2.7	0.022654931
	J00073_at	615	J00073	actin, alpha, cardiac muscle15q11-qter	-2.7	0.029724167
	RC_H05084_at	547	H05084	ESTs, Weakly similar to ORF YDL055c [S.cerevisiae]	-2.7	0.016965435
	AA045870_at	34	AA045870	Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072)	-2.7	0.005480167
	RC_T68873_f_at	911	T68873	metallothionein 1L16q13	-2.7	0.001140431
	RC_N72253_at	778	N72253	ESTs	-2.7	0.001832591
	RC_AA447977_s_at	352	AA447977	Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072)	-2.7	0.001255304
	RC_H18947_at	561	H18947	ESTs	-2.7	0.00193501
	RC_H77597_f_at	594	H77597	metallothionein 1H16q13	-2.7	0.001560766
	RC_H94475_s_at	605	H94475	alpha-2-plasmin inhibitor17pter-p12	-2.6	0.01435663
	RC_AA025370_at	15	AA025370	KIAA0872 protein	-2.6	0.013924142
	RC_AA443114_at	343	AA443114	ESTs, Moderately similar to PIM-1 PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE [M.musculus]	-2.6	0.000703574
	RC_F09684_at	535	F09684	ESTs	-2.6	0.000107291
	RC_AA031360_s_at	20	AA031360	ESTs	-2.6	0.047293081
	RC_AA416685_at	290	AA416685	UNC13 (C. elegans)-like9p11-p12	-2.6	0.023296279
	D29805_at	487	D29805	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 19p13	-2.6	2.3562E-05
	RC_H58873_s_at	583	H58873	solute carrier family 2 (facilitated glucose transporter), member 11p35-p31.3	-2.5	0.000710917
	M10942_at	652	M10942	metallothionein 1E (functional)16q13	-2.5	0.017370635
	RC_T03593_at	875	T03593	ESTs	-2.5	0.006239127
	RC_N95495_at	799	N95495	small inducible cytokine A5 (RANTES)17q11.2-q12	-2.5	0.002392984
	RC_AA017063_r_at	8	AA017063	ESTs, Highly similar to Miz-1 protein [H.sapiens]	-2.5	0.048093776
	RC_R00144_at	801	R00144	ESTs	-2.5	0.018222161
	RC_AA599522_f_at	437	AA599522	squamous cell carcinoma antigen recognised by T cells	-2.5	0.03100833

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_AA219552_s_at	134	AA219552	ESTs	-2.5	0.043156485
	RC_AA447537_at	350	AA447537	ESTs, Moderately similar to (defline not available 5360237) [M.musculus]	-2.5	0.031129269
	RC_AA070752_s_at	51	AA070752	insulin receptor substrate 12q36	-2.5	0.002895462
	RC_R02003_r_at	804	R02003	ESTs, Weakly similar to cappuccino [D.melanogaster]	-2.4	0.002315115
	L13698_at	638	L13698	growth arrest-specific 19q21.3-q22.1	-2.4	0.013393145
	RC_AA432292_at	325	AA432292	ESTs, Moderately similar to B cell growth factor [H.sapiens]	-2.4	0.000956642
	RC_H99648_s_at	613	H99648	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis5q22-q23	-2.4	0.009066307
	RC_AA131919_at	75	AA131919	putative type II membrane protein	-2.4	0.000187872
	RC_AA621695_at	458	AA621695	ESTs	-2.4	0.008761556
	RC_AA598695_at	427	AA598695	ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	-2.4	0.000549977
	RC_AA430388_at	321	AA430388	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	-2.4	0.000135176
	M24069_at	672	M24069	cold shock domain protein A12p13.1	-2.4	0.015890231
	RC_AA434108_at	327	AA434108	Homo sapiens heat shock protein hsp40-3 mRNA, complete cds	-2.4	0.013182623
	RC_AA405488_at	268	AA405488	ESTs	-2.3	0.015044159
	RC_AA419546_at	297	AA419546	ESTs	-2.3	0.030432017
	RC_W38197_at		W38197	EST	-2.3	0.013006462
	RC_R38709_s_at	824	R38709	superoxide dismutase 2, mitochondrial6q25.3	-2.3	0.03567491
	RC_AA121142_at	69	AA121142	ESTs, Moderately similar to copper transport protein HAH1 [H.sapiens]	-2.3	0.043639016
	RC_N26801_at	730	N26801	ESTs	-2.3	0.000580867
	RC_N75960_at	781	N75960	ESTs	-2.3	0.01244791
	RC_R36969_at	820	R36969	ESTs	-2.3	0.019129486
	AA046840_at	36	AA046840	CCAAT/enhancer binding protein (C/EBP), delta8p11.2-p11.1	-2.3	0.002504544
	RC_R46074_at	840	R46074	transforming, acidic coiled-coil containing protein 210q26	-2.3	0.003462273
	X06956_at	1051	X06956	tubulin, alpha 1 (testis specific)2q	-2.3	0.015437809
	RC_H84761_s_at	599	H84761	glutathione peroxidase 13p21.3	-2.2	0.000365528
	RC_W52065_f_at	1012	W52065	KIAA0539 gene product	-2.2	0.016497348
	RC_AA279757_at	192	AA279757	ESTs, Weakly similar to (defline not available 4481810) [D.melanogaster]	-2.2	0.003272622
	RC_H16676_s_at	556	H16676	ESTs, Weakly similar to (defline not available 5107634) [R.norvegicus]	-2.2	8.86866E-05
	RC_AA255480_at	173	AA255480	ESTs	-2.2	0.009359024
	RC_R96924_s_at	866	R96924	ESTs	-2.2	0.000201685
	RC_AA342337_at	231	AA342337	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	-2.2	0.024999347
	RC_AA004699_at	1	AA004699	putative translation initiation factor	-2.2	0.022298405

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_AA401965_at	258	AA401965	tumor suppressor deleted in oral cancer-related 111q13	-2.2	0.006294885
	RC_F02470_at	524	F02470	Homo sapiens clone 24796 mRNA sequence	-2.2	0.022313149
	X76180_at	1086	X76180	sodium channel, nonvoltage-gated 1 alpha12p13	-2.2	0.023078001
	RC_R49138_s_at	841	R49138	coatomer protein complex, subunit epsilon	-2.2	0.020401578
	RC_D80237_s_at	506	D80237	actin related protein 2/3 complex, subunit 4 (20 kD)	-2.2	0.022022634
	RC_AA402224_at	260	AA402224	growth arrest and DNA-damage-inducible, gamma9q22.1-q22.2	-2.2	0.014983528
	RC_AA281599_at	203	AA281599	Homo sapiens mRNA for for histone H2B, clone pjG4-5-14	-2.2	0.029567009
	RC_N78630_at	782	N78630	KIAA0870 protein	-2.2	0.006668895
	X85785_rna1_at	1091	X85785	Duffy blood group1q21-q22	-2.2	0.018706507
	RC_AA412063_at	285	AA412063	ESTs	-2.2	0.000686563
	RC_AA022886_at	14	AA022886	ESTs, Weakly similar to phosphatidylinositol transfer protein [H.sapiens]	-2.2	0.000777067
	RC_N24899_at	726	N24899	ESTs	-2.2	0.030610964
	RC_AA101767_at	66	AA101767	ESTs	-2.2	0.009040467
	RC_AA045503_at	32	AA045503	ESTs, Weakly similar to Homo sapiens p20 protein [H.sapiens]	-2.2	0.021950966
	RC_F10078_at	538	F10078	ESTs	-2.1	0.040699115
	RC_H02308_at	545	H02308	ESTs	-2.1	0.036730715
	RC_AA284153_at	210	AA284153	ESTs	-2.1	0.021270233
	RC_AA453433_at	363	AA453433	HLA-B associated transcript-16p21.3	-2.1	0.013366375
	RC_AA403159_at	265	AA403159	Homo sapiens Ste-20 related kinase SPAK mRNA, complete cds	-2.1	0.025212073
	RC_T17428_s_at	883	T17428	Homo sapiens clone 23836 mRNA sequence	-2.1	0.044754602
	RC_W92449_at	1037	W92449	ESTs, Highly similar to (defline not available 4587714) [H.sapiens]	-2.1	0.019386585
	RC_AA609312_at	443	AA609312	ESTs	-2.1	0.003204911
	D28589_at	486	D28589	Human mRNA (KIAA00167), partial sequence	-2.1	0.000408478
	RC_AA232508_at	139	AA232508	ESTs, Highly similar to (defline not available 4929647) [H.sapiens]	-2.1	0.004626663
	RC_AA280929_s_at	199	AA280929	ESTs	-2.1	0.028189798
	W63793_at	1020	W63793	S-adenosylmethionine decarboxylase 16q21-q22	-2.1	0.032076011
	RC_R36881_s_at	819	R36881	Homo sapiens DNA from chromosome 19-cosmid R30879 containing USF2, genomic sequence	-2.1	0.007343473
	RC_AA278767_s_at	188	AA278767	ESTs	-2.1	0.001983494
	RC_R98442_at	867	R98442	ESTs	-2.1	0.007227226
	X99728_at	1098	X99728	H.sapiens NDUFV3 gene, exon 3.	-2.1	0.001404191
	RC_R09379_at	807	R09379	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 212q13	-2.1	0.006004344

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_R99092_at	868	R99092	EST, Moderately similar to (defline not available 5052951) [H.sapiens]	-2.1	0.016256526
	X95325_s_at	1095	X95325	cold shock domain protein A12p13.1	-2.1	0.025953179
	RC_T56281_f_at	902	T56281	Human metallothionein (MT)I-F gene	-2.1	0.032089569
	RC_R44397_at	835	R44397	ESTs	-2.1	0.000265391
	RC_H27180_f_at	568	H27180	ESTs	-2.1	0.004317675
	AA165312_at	103	AA165312	ESTs	-2.1	0.025559572
	RC_AA279313_s_at	191	AA279313	methyl CpG binding protein 2Xq28	-2.1	0.030594523
	HG4322-HT4592_at	465	AF141349	Homo sapiens beta-tubulin mRNA, complete cds.	-2.1	0.017120749
	RC_H81413_f_at	597	H81413	high-mobility group (nonhistone chromosomal) protein isoforms I and Y6p21	-2.1	0.009976588
	RC_W94333_at	1039	W94333	ESTs, Highly similar to (defline not available 5107163) [H.sapiens]	-2.1	0.000435688
	RC_AA455070_at	369	AA455070	eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD)	-2.1	0.025226928
	RC_R11526_f_at	809	R11526	parathymosin17q12-q22	-2.1	0.027182202
	RC_T15409_f_at	877	T15409	EST	-2.1	0.001478856
	RC_H05625_f_at	548	H05625	ESTs	-2.1	0.024564209
	RC_AA620461_at	452	AA620461	ESTs	-2.0	0.022844667
	RC_AA449791_f_at	356	AA449791	EST	-2.0	0.025394324
	RC_AA435769_s_at	330	AA435769	ESTs	-2.0	0.008375153
	RC_N55502_at	755	N55502	ESTs	-2.0	0.021894439
	AF001294_at	463	AF001294	tumor suppressing subtransferable candidate 311p15.5	-2.0	0.03566128
	RC_Z40898_at	1118	Z40898	ESTs, Highly similar to (defline not available 4929639) [H.sapiens]	-2.0	0.002289892
	RC_AA436861_at	340	AA436861	ESTs	-2.0	0.00187676
	M63573_at	697	M63573	peptidylprolyl isomerase B (cyclophilin B)15	-2.0	0.044239663
	RC_T25732_f_at	888	T25732	KIAA0252 protein	-2.0	0.041237995
	RC_R01257_at	803	R01257	ESTs, Weakly similar to (defline not available 4456991) [H.sapiens]	-2.0	0.005735841
	RC_H91703_i_at	603	H91703	cell division cycle 2717q12-17q23.2	-2.0	0.001412925
	RC_N34817_at	739	N34817	ESTs	-2.0	0.040996591
	RC_R60777_at	850	R60777	ESTs, Weakly similar to KIAA0374 [H.sapiens]	-2.0	0.000245565
	RC_AA386264_at	245	AA386264	ESTs, Weakly similar to MICROTUBULE-ASSOCIATED PROTEIN 1B [M.musculus]	-2.0	0.000541139
	RC_AA251769_at	168	AA251769	ESTs, Weakly similar to Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [H.sapiens]	-2.0	0.008985897
	RC_R56602_at	846	R56602	Ig superfamily proteinXq12-q13.3	-2.0	0.024051216
	RC_AA397919_at	247	AA397919	ESTs	-2.0	0.029784087

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms 1669617.1

	Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-change N1-N2 vs With	p-value N1-N2 vs With
Up-regulated	RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	22.5	0.025197485
	RC_W37778_f_at	1002	W37778	ESTs, Weakly similar to envelope protein [H.sapiens]	-2.0	0.043013942
	AA248555_at	164	AA248555	ESTs	-2.0	0.000824698
	RC_AA463693_at	385	AA463693	ESTs, Weakly similar to SERINE/THREONINE-PROTEIN KINASE NEK3 [H.sapiens]	-2.0	0.002809026
	W76181_at	1030	W76181	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)5q31	-2.0	0.008370263
	RC_AA171939_at	106	AA171939	ESTs	-2.0	0.015796116
	U30999_at	961	U30999	U30999 Homo sapiens MV3 melanoma Homo sapiens cDNA clone memd	-2.0	0.007070546
	RC_F03254_f_at	527	F03254	synuclein, alpha (non A4 component of amyloid precursor)4q21	-2.0	0.011479379
	RC_H26288_at	567	H26288	ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	-2.0	0.000262324
	RC_AA007158_f_at	4	AA007158	ESTs	-2.0	0.001870921
	RC_Z38785_at	1109	Z38785	Homo sapiens clone 23940 mRNA sequence	-2.0	0.013437083
	RC_AA282247_at	204	AA282247	ESTs	-2.0	0.000515617
	RC_T23935_s_at	887	T23935	ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]	-2.0	0.006493804
	RC_R59593_at	848	R59593	ESTs	-2.0	0.014592934
	RC_AA446241_at	345	AA446241	tropomyosin 2 (beta)9p13.2-p13.1	-2.0	0.040680667
	RC_Z40556_at	1116	Z40556	DJ222E13.1a.1 (C-terminal part of novel protein dJ222E13.1) (partial isoform 1)	-2.0	0.019444878
	RC_AA159025_at	100	AA159025	ESTs, Highly similar to (defline not available 4680655) [H.sapiens]	-2.0	0.01375696
	RC_H03387_s_at	546	H03387	estrogen-responsive B box protein17p11.2	-2.0	0.036382844
	RC_H17333_at	558	H17333	EST	-2.0	0.018111182
	RC_AA412722_s_at	289	AA412722	putative cyclin G1 interacting protein7	-2.0	0.006838915
	U65579_at	979	U65579	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)11q13	-2.0	0.013707565
	RC_R88209_at	860	R88209	ESTs	-2.0	0.040272012
	RC_Z38266_at	1106	Z38266	Homo sapiens PAC clone DJ0777O23 from 7p14-p15	-2.0	0.009414008

Patent Pending

Table 2 **Normal1-Normal2 vs BPH-Cancer (Up-regulated)** 1669988.1

Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
V01512_rna1_at	993	V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.0	0.001216643
RC_T90619_f_at	926	T90619	actin, gamma 117q25	15.7	0.044124187
U20734_s_at	952	U20734	jun B proto-oncogene19p13.2	14.3	0.004404553
U62015_at	978	U62015	insulin-like growth factor binding protein 101p22-p31	13.8	0.000487216
AA374109_at	241	AA374109	ESTs, Moderately similar to (defline not available 5031506) [R.norvegicus]	13.0	0.025911461
RC_T79768_at	914	T79768	ESTs	12.2	0.018940142
RC_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21	11.1	0.046025784
X52541_at	1064	X52541	early growth response 15q31.1	9.7	0.003167537
RC_N66802_at	767	N66802	early growth response 38p23-p21	9.7	0.026764792
RC_AA463726_s_at	386	AA463726	JM27 proteinXp11.23	9.4	0.003409168
N40141_at	743	N40141	JM27 proteinXp11.23	8.4	0.021768214
M34996_s_at	685	M34996	major histocompatibility complex, class II, DQ alpha 16p21.3	7.7	0.015886207
RC_T67053_f_at	909	T67053	immumoglobulin lambda gene cluster22q11.1-q11.2	7.4	0.000196865
RC_AA404957_at	266	AA404957	ESTs, Highly similar to MATRIX GLA-PROTEIN PRECURSOR [H.sapiens]	6.6	0.011451385
RC_H64493_f_at	590	H64493	immunoglobulin gamma 3 (Gm marker)14q32.33	6.5	0.002716347
RC_N47686_s_at	744	N47686	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)18q11-q12	6.3	0.015568892
RC_W44760_s_at	1006	W44760	frizzled-related protein2qter	6.3	0.016891036
L19871_at	642	L19871	activating transcription factor 3	6.2	0.007603286
M92934_at	708	M92934	connective tissue growth factor6q23.1	6.1	0.001046931
M62831_at	695	M62831	immediate early protein19	5.8	0.00753286
L22524_s_at	643	L22524	matrix metalloproteinase 7 (matrilysin, uterine)11q21-q22	5.8	0.048289798
J03507_at	621	J03507	complement component 75p13	5.6	0.00240657
RC_AA236455_r_at	153	AA236455	ESTs	5.5	0.022653542
RC_AA450127_at	359	AA450127	growth arrest and DNA-damage-inducible, beta19p13.3	5.5	0.023227588
RC_AA281345_f_at	201	AA281345	immediate early protein19	5.4	0.003661068
RC_N30198_at	733	N30198	ESTs	5.3	0.005657756
AFFX-HSAC07/X00351_5_at	1040	X00351	Human mRNA for beta-actin	5.3	0.01547291
D83018_at	513	D83018	nel (chicken)-like 212q13.11-q13.12	5.1	0.003774757
J04111_at	624	J04111	Jun activation domain binding protein1p32-p31	5.0	0.000243067
X51345_at	1062	X51345	jun B proto-oncogene19p13.2	5.0	0.017173421
RC_AA398903_at	250	AA398903	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	4.9	0.014577818
RC_H17550_at	559	H17550	ESTs	4.7	0.012079391
S81914_at	873	S81914	immediate early response 36p21.3	4.5	0.006218653
RC_AA250958_f_at	167	AA250958	EST	4.4	1.88343E-05

Table 2 **Normal1-Normal2 vs BPH-Cancer (Up-regulated)** 1669988.1

Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
RC_AA446651_at	346	AA446651	ESTs	4.4	0.026022802
HG1872-HT1907_at	674	M28590	Human (clone pcDG-79) MHC HLA-DG protein 41 mRNA, partial cds.	4.3	0.008830524
RC_AA490667_at	419	AA490667	ESTs	4.3	0.048863016
RC_N67041_at	768	N67041	ESTs	4.1	0.009333688
V00563_at	991	V00563	immunoglobulin mu14q32.33	4.1	0.004301939
X57809_s_at	1069	X57809	immumoglobulin lambda gene cluster22q11.1-q11.2	4.1	0.025371658
R69417_at	852	R69417	ESTs	4.1	0.046373179
J00231_f_at	617	J00231	immunoglobulin gamma 3 (Gm marker)14q32.33	4.0	0.004766015
RC_AA402903_f_at	263	AA402903	immunoglobulin gamma 3 (Gm marker)14q32.33	3.9	0.000172905
U21128_at	953	U21128	lumican12q21.3-q22	3.9	0.000708917
M12529_at	655	M12529	apolipoprotein E19q13.2	3.7	0.026856247
RC_AA436616_at	335	AA436616	ESTs	3.7	0.020860083
U72649_at	983	U72649	B-cell translocation gene 2 (pheochromacytoma cell-3)1q32	3.7	0.002487396
X03689_s_at	1044	X03689	Human mRNA fragment for elongation factor TU (N-terminus)	3.7	0.04821902
AFFX-HSAC07/X00351_5_at	1040	X00351	Human mRNA for beta-actin	3.6	0.029717275
RC_T62857_at	903	T62857	ESTs	3.6	0.002846539
Z74616_s_at	1123	Z74616	collagen, type I, alpha 27q22.1	3.6	0.004328291
X06700_s_at	1049	X06700	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)2q31	3.6	0.010596098
RC_H86112_f_at	600	H86112	KIAA0471 gene product1q24-q25	3.6	0.017013968
M57466_s_at	690	M57466	major histocompatibility complex, class II, DP beta 16p21.3	3.5	0.005924671
RC_F09281_at	533	F09281	ESTs	3.5	0.006841731
RC_R51831_at	843	R51831	ESTs	3.4	0.000941423
RC_H21814_f_at	563	H21814	immumoglobulin lambda gene cluster22q11.1-q11.2	3.4	0.009767098
RC_W86513_at	1033	W86513	ESTs	3.4	0.003776481
RC_H40424_s_at	572	H40424	EST	3.4	0.016283906
X57025_at	1066	X57025	insulin-like growth factor 1 (somatomedin C)12q22 q23	3.3	0.040489253
RC_AA044219_at	29	AA044219	BK984G1.1 (PUTATIVE C-terminal end of a novel protein with Collagen triple helix repeats)	3.3	0.001761114
RC_AA028092_s_at	17	AA028092	transcription factor 216pter-qter	3.3	0.003405482
RC_AA446661_at	347	AA446661	ESTs	3.3	0.041188995
RC_D80063_f_at	505	D80063	ESTs	3.3	0.049585142
M92843_s_at	707	M92843	zinc finger protein homologous to Zfp-36 in mouse19q13.1	3.3	0.006174082
M34516_r_at	684	M34516	immunoglobulin lambda-like polypeptide 322q11.2	3.2	0.02344053

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Table 2 **Normal1-Normal2 vs BPH-Cancer (Up-regulated)** 1669988.1

Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
M87789_s_at	704	M87789	immunoglobulin gamma 3 (Gm marker)14q32.33	3.2	0.004534646
N75870_s_at	780	N75870	dual specificity phosphatase 15q34	3.2	0.000157434
RC_AA609309_at	442	AA609309	ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]	3.1	0.03780658
S59049_at	870	S59049	regulator of G-protein signalling 11q31	3.0	0.002419303
AFFX-HUMGAPDH/M33197_5_at	679	M33197	Human GAPDH	3.0	0.034538288
RC_D51060_s_at	495	D51060	Jun activation domain binding protein1p32-p31	3.0	0.022390037
RC_T23468_at	884	T23468	ESTs	2.9	0.001634616
U30521_at	960	U30521	P311 protein	2.9	0.009484198
Z48501_s_at	1121	Z48501	poly(A)-binding protein-like 13q22-q25	2.9	0.026396977
W73859_at	1028	W73859	transcription factor 216pter-qter	2.9	0.037326183
AA093923_at	63	AA093923	tissue inhibitor of metalloproteinase 217q25	2.8	0.041564022
RC_AA236476_at	154	AA236476	ESTs, Weakly similar to (defline not available 4507549) [H.sapiens]	2.7	0.038305276
U10550_at	944	U10550	GTP-binding protein overexpressed in skeletal muscle8q13-q21	2.7	0.040657885
RC_N24902_at	727	N24902	E1B-55kDa-associated protein 5	2.7	0.03810507
RC_AA056121_at	46	AA056121	ESTs	2.7	0.024285705
RC_H98835_at	611	H98835	ESTs	2.7	0.019901442
K02405_f_at	629	K02405	Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds	2.7	0.00138806
U90552_s_at	988	U90552	butyrophilin, subfamily 3, member A16p23	2.7	3.91186E-05
RC_N59831_at	759	N59831	ESTs	2.7	0.04543669
L33799_at	645	L33799	procollagen C-endopeptidase enhancer7q22	2.7	0.010879277
RC_N59532_s_at	758	N59532	aminomethyltransferase (glycine cleavage system protein T)3p21.2-p21.1	2.6	0.025712285
D13628_at	476	D13628	angiopoietin 18q22.3-q23	2.6	0.027204836
AA156897_s_at	97	AA156897	Homo sapiens mRNA; cDNA DKFZp564I1922 (from clone DKFZp564I1922)	2.6	0.001580022
RC_N67876_s_at	773	N67876	insulin-like growth factor 1 (somatomedin C)12q22 q23	2.6	0.03992641
M73720_at	702	M73720	carboxypeptidase A3 (mast cell)3q21-q25	2.6	0.023298997
H49440_at	578	H49440	nudix (nucleoside diphosphate linked moiety X)-type motif 36p21.2	2.6	0.002498701
RC_AA250850_at	166	AA250850	adrenergic, beta, receptor kinase 222q11	2.5	0.041156086
RC_T49061_at	894	T49061	ESTs	2.5	0.00934004
W28214_at	996	W28214	ESTs	2.5	0.037677921
RC_H44631_s_at	573	H44631	immediate early protein19	2.5	0.0423037
D28137_at	484	D28137	bone marrow stromal cell antigen 219p13.2	2.5	0.026212334
RC_AA609027_at	441	AA609027	ESTs	2.5	0.038550623
RC_AA257093_r_at	178	AA257093	T-cell receptor, beta cluster7q35	2.4	0.002653232
RC_F13763_at	542	F13763	ESTs	2.4	0.016949277
RC_H08548_s_at	550	H08548	ATP citrate lyase17q12-q21	2.4	0.036998522
RC_AA436618_at	336	AA436618	ESTs	2.4	0.001789907

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Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
RC_W45664_s_at	1008	W45664	5' nucleotidase (CD73)6q14-q21	2.4	0.001762727
AA082546_at	54	AA082546	ESTs	2.4	0.021791878
D10522_at	471	D10522	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)6q22.2	2.4	0.017333686
RC_AA411860_at	280	AA411860	ESTs, Highly similar to (defline not available 4929723) [H.sapiens]	2.4	0.02766922
AB002340_at	461	AB002340	KIAA0342 gene product	2.3	0.003238699
U53445_at	972	U53445	downregulated in ovarian cancer 13	2.3	0.009361652
AA091278_at	60	AA091278	ESTs	2.3	0.046253689
RC_AA486072_i_at	410	AA486072	small inducible cytokine A5 (RANTES)17q11.2-q12	2.3	0.012816473
RC_T53590_s_at	899	T53590	cytochrome P450, subfamily XIA (cholesterol side chain cleavage)15q23-q24	2.3	4.29636E-05
RC_N91971_f_at	791	N91971	retinol-binding protein 1, cellular3q23	2.3	0.025171598
RC_AA043777_at	28	AA043777	ESTs	2.3	0.004490188
RC_H54764_at	580	H54764	EST, Weakly similar to X-linked retinopathy protein {C-terminal, clone XEH.8c} [H.sapiens]	2.3	0.036980431
RC_AA443923_at	344	AA443923	ESTs	2.3	0.025833241
U60975_at	977	U60975	Homo sapiens gp250 precursor, mRNA, complete cds.	2.3	0.041238204
M34516_at	684	M34516	immunoglobulin lambda-like polypeptide 322q11.2	2.3	0.041388637
RC_N36001_at	740	N36001	ESTs, Weakly similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens]	2.2	0.000449076
AF010193_at	464	AF010193	MAD (mothers against decapentaplegic, Drosophila) homolog 718	2.2	0.005397771
AFFX-HSAC07/X00351_5_at	1040	X00351	Human mRNA for beta-actin	2.2	0.037852217
RC_AA158262_s_at	99	AA158262	calpastatin5q14-q22	2.2	0.006648962
RC_AA156565_at	96	AA156565	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like 122q12	2.2	0.020901922
Z11793_at	1104	Z11793	selenoprotein P, plasma, 15q31	2.2	0.00118281
RC_D80059_s_at	504	D80059	ESTs	2.2	0.033534432
RC_AA450324_at	360	AA450324	ESTs	2.2	0.024832006
RC_N39415_at	742	N39415	osteoglycin (osteoinductive factor)	2.2	0.032001116
RC_T23622_at	886	T23622	ESTs	2.2	0.040417825
RC_AA599365_at	434	AA599365	decorin12q23	2.2	0.011325181
X62320_at	1073	X62320	granulin17	2.2	0.043043858
RC_R85291_at	859	R85291	ESTs	2.2	0.004987693
M11313_s_at	654	M11313	alpha-2-macroglobulin12p13.3-p12.3	2.2	0.011545737
AA047151_at	37	AA047151	ESTs	2.2	0.033987576
RC_AA205724_at	123	AA205724	ESTs	2.2	0.004569368
RC_AA086264_i_at	59	AA086264	ESTs, Highly similar to (defline not available 4191348) [H.sapiens]	2.2	0.020637423
RC_R42424_at	832	R42424	ESTs	2.2	0.033603417
RC_AA347359_s_at	233	AA347359	lysozyme (renal amyloidosis)12	2.1	0.028764499

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Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
AA092716_at	62	AA092716	HLA-B associated transcript-36p21.3	2.1	0.031717351
RC_R42241_at	830	R42241	ESTs	2.1	0.008013968
RC_N57577_at	756	N57577	KIAA0663 gene product	2.1	0.032028875
RC_W67577_s_at	1022	W67577	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)5q32	2.1	0.002072118
C02016_at	466	C02016	KIAA0447 gene product	2.1	0.002399894
RC_AA256268_at	175	AA256268	ESTs	2.1	0.0269568
RC_T96171_at	930	T96171	EST	2.1	0.012219229
X72841_at	1083	X72841	retinoblastoma-binding protein 7	2.1	0.033774692
RC_R45698_at	839	R45698	ESTs	2.1	0.049975895
RC_N22006_s_at	719	N22006	EST	2.1	0.011131338
RC_N69222_at	777	N69222	ESTs	2.1	0.022256915
RC_H97538_at	607	H97538	ESTs	2.0	0.03795259
RC_AA039935_at	23	AA039935	dynein light chain, outer arm 422q12.3-q13.2	2.0	0.011488766
RC_AA084138_at	55	AA084138	ESTs	2.0	0.011124432
AB002379_at	462	AB002379	KIAA0381 protein	2.0	0.000530413
RC_AA460651_at	379	AA460651	heterogeneous nuclear protein similar to rat helix destabilizing protein10	2.0	0.027697892
RC_W02204_at	994	W02204	solute carrier family 24 (sodium/potassium/calcium exchanger), member 115q22	2.0	0.00115779
Y08614_at	1101	Y08614	exportin 1 (CRM1, yeast, homolog)2p16	2.0	0.035368368
D31134_at	488	D31134	KIAA1075 protein	2.0	0.021196526
M94880_f_at	711	M94880	major histocompatibility complex, class I, A6p21.3	2.0	0.025382167
J03040_at	619	J03040	secreted protein, acidic, cysteine-rich (osteonectin)5q31.3-q32	2.0	0.035472553
RC_N68350_at	775	N68350	ESTs	2.0	0.042917893
RC_H48793_at	577	H48793	EST	2.0	0.00296551
HG3543-HT3739_at	675	M29645	insulin-like growth factor 2 (somatomedin A)11p15.5	2.0	0.019712374
RC_W33172_at	999	W33172	ESTs, Weakly similar to ORF2 [M.musculus]	2.0	0.006454106
RC_R08850_at	806	R08850	ESTs	2.0	0.011364766
W52638_at	1014	W52638	ESTs	2.0	0.010612401
M19045_f_at	662	M19045	lysozyme (renal amyloidosis)12	2.0	0.004561974
RC_AA312946_s_at	228	AA312946	ESTs	2.0	0.020272205
RC_AA235310_at	148	AA235310	ESTs	2.0	0.011954937
X03100_cds2_at	1043	X03100	Human mRNA for SB classII histocompatibility antigen alpha-chain	2.0	0.002404541
RC_T16282_f_at	881	T16282	wee1+ (S. pombe) homolog11p15.3-p15.1	2.0	0.031472155
RC_H66642_f_at	591	H66642	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	2.0	0.02460529
RC_AA342337_at	231	AA342337	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	-23.7	3.26344E-05

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L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
RC_AA398908_at	251	AA398908	Human Chromosome 16 BAC clone CIT987SK-A-61E3	-21.7	0.040053626
RC_H15143_s_at	554	H15143	Human clone 23575 mRNA, partial cds	-13.8	0.028261625
RC_N80129_i_at	785	N80129	metallothionein 1L16q13	-12.6	0.002146038
RC_AA465394_at	390	AA465394	ESTs	-12.6	0.004961162
RC_AA236545_at	156	AA236545	ESTs	-12.5	0.034938167
RC_W42778_at	1004	W42778	Homo sapiens clone 24636 mRNA sequence	-12.3	0.010449419
RC_T40895_at	892	T40895	ESTs	-12.0	0.01968535
RC_H94475_s_at	605	H94475	alpha-2-plasmin inhibitor17pter-p12	-11.7	0.012919819
RC_R71792_s_at	855	R71792	ESTs, Moderately similar to FAT-SPECIFIC PROTEIN FSP27 [M.musculus]	-10.4	0.002540356
RC_AA609006_at	440	AA609006	ESTs	-7.5	0.013902978
RC_AA026641_s_at	16	AA026641	secretory leukocyte protease inhibitor (antileukoproteinase)	-7.0	0.01850877
X65614_at	1076	X65614	S100 calcium-binding protein P4p16	-6.7	0.005634308
X93036_at	1093	X93036	phospholemman-like, expressed in breast tumors, 8kD	-6.6	0.005278275
RC_T94447_s_at	928	T94447	ESTs, Moderately similar to (defline not available 4335935) [M.musculus]	-5.7	0.006891909
RC_AA405488_at	268	AA405488	ESTs	-5.5	0.00023986
RC_T73433_s_at	912	T73433	angiotensinogen1q41-qter	-5.5	0.009418205
M99487_at	716	M99487	folate hydrolase (prostate-specific membrane antigen) 111p11.2	-5.3	0.008067789
RC_W88568_at	1035	W88568	glycogenin 2Xp22.3	-5.1	0.024739084
RC_AA460914_at	380	AA460914	ESTs	-5.0	0.024385552
X57129_at	1067	X57129	H1 histone family, member 26p21.3	-4.8	0.006322499
RC_Z41642_at	1119	Z41642	ESTs	-4.7	0.009525521
RC_R46074_at	840	R46074	transforming, acidic coiled-coil containing protein 210q26	-4.7	0.001327844
J03910_rna1_at	622	J03910	metallothionein 1G16q13	-4.6	0.004574277
RC_AA350265_at	237	AA350265	histone deacetylase A	-4.5	0.002897414
AA165312_at	103	AA165312	ESTs	-4.2	0.005487803
RC_AA419011_at	296	AA419011	Homo sapiens mRNA; cDNA DKFZp586D0823 (from clone DKFZp586D0823)	-4.0	0.019079557
RC_N92502_s_at	794	N92502	ESTs, Moderately similar to HERV-E integrase [H.sapiens]	-4.0	0.030144039
RC_F03969_at	528	F03969	ESTs, Weakly similar to tumorous imaginal discs protein Tid56 homolog [H.sapiens]	-4.0	0.017024613
X76717_at	1087	X76717	metallothionein 1L16q13	-3.9	0.001145402
RC_AA416762_s_at	291	AA416762	nuclear receptor subfamily 1, group H, member 219q13.3-19q13.3	-3.8	0.011735303
RC_AA053424_at	40	AA053424	ESTs, Weakly similar to mucin Muc3 [R.norvegicus]	-3.8	0.009737433
X64177_f_at	1075	X64177	metallothionein 1H16q13	-3.7	0.003297195
RC_N32748_at	736	N32748	ESTs	-3.6	0.021454174
RC_AA416685_at	290	AA416685	UNC13 (C. elegans)-like9p11-p12	-3.6	0.016338392
RC_AA505136_at	426	AA505136	ESTs	-3.5	0.007200396
RC_AA165313_at	104	AA165313	ESTs	-3.5	0.037649191

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RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
RC_F02245_at	522	F02245	monoamine oxidase AXp11.4-p11.3	-3.4	0.005486135
RC_AA004699_at	1	AA004699	putative translation initiation factor	-3.4	0.00057505
RC_AA599331_at	433	AA599331	ESTs	-3.4	0.01136457
RC_N26904_at	731	N26904	ESTs, Weakly similar to FK506/rapamycin-binding protein FKBP13 precursor [H.sapiens]	-3.3	0.045410608
RC_AA070752_s_at	51	AA070752	insulin receptor substrate 12q36	-3.3	0.028433761
RC_AA599522_f_at	437	AA599522	squamous cell carcinoma antigen recognised by T cells	-3.2	0.005311305
RC_N94303_at	797	N94303	ESTs	-3.1	0.000160723
RC_F10078_at	538	F10078	ESTs	-3.1	0.022464594
RC_AA447537_at	350	AA447537	ESTs, Moderately similar to (defline not available 5360237) [M.musculus]	-3.1	0.007323728
L77701_at	651	L77701	human homolog of yeast mitochondrial copper recruitment gene	-3.0	0.001489928
RC_H27675_at	569	H27675	ESTs	-3.0	0.016160504
V00594_at	992	V00594	metallothionein 2A16q13	-2.9	0.001495259
U52969_at	970	U52969	Purkinje cell protein 421q22.2-q22.3	-2.9	6.3447E-05
RC_R42607_at	834	R42607	ESTs	-2.8	0.008960052
RC_AA451836_at	362	AA451836	ESTs	-2.7	0.008401586
RC_F04492_at	531	F04492	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	-2.7	0.001443051
RC_H77597_f_at	594	H77597	metallothionein 1H16q13	-2.7	0.00332868
RC_AA430388_at	321	AA430388	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	-2.7	0.000114004
RC_T90190_s_at	925	T90190	H1 histone family, member 26p21.3	-2.7	0.030242714
RC_H16171_f_at	555	H16171	cleft lip and palate associated transmembrane protein 119q13.2-q13.3	-2.7	0.023414443
RC_AA022886_at	14	AA022886	ESTs, Weakly similar to phosphatidylinositol transfer protein [H.sapiens]	-2.7	0.00489294
RC_R28370_at	815	R28370	ESTs	-2.7	0.003724547
RC_AA261907_at	182	AA261907	ESTs, Weakly similar to (defline not available 3874144) [C.elegans]	-2.6	0.043689441
RC_W37778_f_at	1002	W37778	ESTs, Weakly similar to envelope protein [H.sapiens]	-2.6	0.030756837
RC_T98019_at	932	T98019	EST, Highly similar to PEREGRIN [H.sapiens]	-2.5	0.035566681
RC_N33927_s_at	737	N33927	H2B histone family, member B6p21.3	-2.5	0.013093926
RC_R40431_at	828	R40431	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016)	-2.5	0.004235538
RC_AA133756_at	78	AA133756	Rho-associated, coiled-coil containing protein kinase 22p24	-2.5	0.012389163
RC_AA152200_s_at	92	AA152200	ESTs	-2.5	0.004366137
W63793_at	1020	W63793	S-adenosylmethionine decarboxylase 16q21-q22	-2.5	0.005714247
RC_AA410298_at	274	AA410298	ESTs	-2.5	0.018744617
X99728_at	1098	X99728	H.sapiens NDUFV3 gene, exon 3	-2.5	0.004580383
RC_W78127_at	1031	W78127	ESTs, Weakly similar to KIAA0425 [H.sapiens]	-2.5	0.001240164

Table 2 **Normal1-Normal2 vs BPH-Cancer (Up-regulated)** 1669988.1

Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
RC_R96924_s_at	866	R96924	ESTs	-2.5	0.006515911
RC_H16768_at	557	H16768	ESTs	-2.5	0.005669237
X76180_at	1086	X76180	sodium channel, nonvoltage-gated 1 alpha12p13	-2.5	0.007625025
RC_AA432162_at	324	AA432162	Homo sapiens mRNA; cDNA DKFZp586B2022 (from clone DKFZp586B2022)	-2.4	0.010199113
RC_H88798_at	602	H88798	ESTs	-2.4	0.000783143
RC_AA609312_at	443	AA609312	ESTs	-2.4	0.016243321
RC_AA131919_at	75	AA131919	putative type II membrane protein	-2.4	0.000264791
RC_N80129_f_at	785	N80129	metallothionein 1L16q13	-2.4	0.002297016
RC_AA182030_at	110	AA182030	ESTs	-2.4	0.041632378
W70167_at	1025	W70167	ESTs	-2.4	0.00395969
RC_AA599522_r_at	437	AA599522	squamous cell carcinoma antigen recognised by T cells	-2.4	0.004347078
RC_N52254_s_at	749	N52254	SH3-binding domain glutamic acid-rich protein21q22.3	-2.4	0.011171389
RC_N95495_at	799	N95495	small inducible cytokine A5 (RANTES)17q11.2-q12	-2.4	0.002430242
RC_T68873_f_at	911	T68873	metallothionein 1L16q13	-2.4	0.00320019
AA429539_f_at	318	AA429539	ESTs	-2.4	0.020751882
RC_AA435769_s_at	330	AA435769	ESTs	-2.4	0.009832353
RC_AA029356_at	18	AA029356	ESTs	-2.3	0.007208722
AA316686_s_at	229	AA316686	ESTs, Highly similar to huntingtin interacting protein HYPK [H.sapiens]	-2.3	0.000225753
RC_H02308_at	545	H02308	ESTs	-2.3	0.041776289
RC_AA258476_at	179	AA258476	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)	-2.3	0.02070961
X06956_at	1051	X06956	tubulin, alpha 1 (testis specific)2q	-2.3	0.003656874
RC_H99694_at	614	H99694	ESTs	-2.3	0.013645335
RC_AA479044_s_at	402	AA479044	ESTs, Weakly similar to PROGASTRICSIN PRECURSOR [H.sapiens]	-2.3	0.047032301
RC_AA436861_at	340	AA436861	ESTs	-2.3	0.001794201
M24069_at	672	M24069	cold shock domain protein A12p13.1	-2.3	0.014123514
RC_AA410311_at	275	AA410311	ESTs	-2.3	0.045227011
W52858_at	1015	W52858	Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522)	-2.3	0.002276405
RC_W38197_at		W38197	EST	-2.3	1.96016E-05
J00073_at	615	J00073	actin, alpha, cardiac muscle15q11-qter	-2.3	0.018476889
RC_D51069_f_at	496	D51069	melanoma adhesion molecule	-2.3	0.042693395
RC_AA504805_s_at	424	AA504805	interferon stimulated gene (20kD)15q26	-2.3	0.008805886
RC_F03254_f_at	527	F03254	synuclein, alpha (non A4 component of amyloid precursor)4q21	-2.3	0.003668915
M35252_at	686	M35252	transmembrane 4 superfamily member 3	-2.3	0.028083185
RC_AA040731_at	25	AA040731	ESTs	-2.2	0.028924808
RC_AA496247_at	422	AA496247	ESTs	-2.2	0.013336314
X59766_at	1071	X59766	alpha-2-glycoprotein 1, zinc7	-2.2	0.002003511

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Table 2 **Normal1-Normal2 vs BPH-Cancer (Up-regulated)** 1669988.1

Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
RC_R84421_at	857	R84421	eukaryotic translation elongation factor 1 alpha 16q14	-2.2	0.016333706
AA328993_s_at	230	AA328993	ESTs	-2.2	0.004438605
RC_R44535_f_at	836	R44535	endonuclease G9q34.1	-2.2	0.014319616
U41518_at	964	U41518	aquaporin 1 (channel-forming integral protein, 28kD)7p14	-2.2	0.009447457
RC_W33179_at	1000	W33179	testis-specific kinase 21p32	-2.2	0.001104272
RC_H58873_s_at	583	H58873	solute carrier family 2 (facilitated glucose transporter), member 11p35-p31.3	-2.2	0.000238641
RC_R31679_s_at	816	R31679	ESTs	-2.2	0.01000414
RC_AA189083_at	114	AA189083	ESTs, Highly similar to (defline not available 4589468) [M.musculus]	-2.2	0.002468046
RC_AA251769_at	168	AA251769	ESTs, Weakly similar to Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [H.sapiens]	-2.2	0.010819016
RC_W70131_at	1024	W70131	ESTs	-2.2	0.02955725
RC_R09379_at	807	R09379	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 212q13	-2.2	0.009730513
RC_AA621695_at	458	AA621695	ESTs	-2.1	0.001994051
RC_H18947_at	561	H18947	ESTs	-2.1	0.027246274
RC_AA219552_s_at	134	AA219552	ESTs	-2.1	0.046510941
RC_N22620_at	722	N22620	ESTs	-2.1	0.013527392
RC_R02003_r_at	804	R02003	ESTs, Weakly similar to cappuccino [D.melanogaster]	-2.1	0.010597095
RC_AA405559_at	270	AA405559	ESTs	-2.1	0.009305601
RC_AA463693_at	385	AA463693	ESTs, Weakly similar to SERINE/THREONINE-PROTEIN KINASE NEK3 [H.sapiens]	-2.1	0.004156996
RC_AA481407_at	405	AA481407	ESTs	-2.1	0.002741696
M11119_at	653	M11119	Human endogenous retrovirus envelope region mRNA (PL1)	-2.1	0.003718876
RC_AA159025_at	100	AA159025	ESTs, Highly similar to (defline not available 4680655) [H.sapiens]	-2.1	0.011127532
RC_AA411981_at	283	AA411981	ESTs, Weakly similar to putative seven pass transmembrane protein [H.sapiens]	-2.1	0.044294612
RC_W57931_at	1017	W57931	ESTs, Moderately similar to CATHEPSIN D PRECURSOR [H.sapiens]	-2.1	0.000755739
X66899_at	1081	X66899	Ewing sarcoma breakpoint region 122q12	-2.1	0.002068901
RC_R49327_at	842	R49327	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 212q13	-2.1	0.030928835
RC_AA609645_at	445	AA609645	eukaryotic translation initiation factor 4 gamma, 13q27-qter	-2.1	0.04955957
RC_AA434108_at	327	AA434108	Homo sapiens heat shock protein hsp40-3 mRNA, complete cds	-2.1	0.034468752
X17567_s_at	1061	X17567	small nuclear ribonucleoprotein polypeptides B and B120	-2.1	0.014475221

Table 2 **Normal1-Normal2 vs BPH-Cancer (Up-regulated)** 1669988.1

Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
J04164_at	626	J04164	interferon-induced protein 17	-2.1	0.023410352
RC_AA135929_s_at	80	AA135929	ESTs, Highly similar to (defline not available 4103057) [M.musculus]	-2.1	0.003009065
L04270_at	634	L04270	lymphotoxin beta receptor (TNFR superfamily, member 312p13	-2.1	0.006776988
RC_H99035_at	612	H99035	ESTs	-2.1	0.001053884
M64673_at	698	M64673	heat shock transcription factor 1	-2.1	0.004283001
X85785_rna1_at	1091	X85785	Duffy blood group1q21-q22	-2.1	0.00657464
M68864_at	700	M68864	Human ORF mRNA, complete cds	-2.1	0.010185833
D50928_at	494	D50928	KIAA0138 gene product	-2.1	0.002283064
RC_AA282247_at	204	AA282247	ESTs	-2.0	0.007970044
RC_R00144_at	801	R00144	ESTs	-2.0	0.006939854
RC_AA485965_at	409	AA485965	ESTs, Highly similar to (defline not available 4336766) [H.sapiens]	-2.0	0.000405037
S45630_at	869	S45630	crystallin, alpha B11q22.3-q23.1	-2.0	0.006157273
RC_T89703_at	923	T89703	ESTs, Highly similar to (defline not available 4455129) [H.sapiens]	-2.0	0.000286616
RC_Z38785_at	1109	Z38785	Homo sapiens clone 23940 mRNA sequence	-2.0	0.00706437
X85373_at	1090	X85373	small nuclear ribonucleoprotein polypeptide G	-2.0	6.93881E-05
RC_F04816_at	532	F04816	ESTs	-2.0	0.005353184
RC_AA043349_at	27	AA043349	ESTs	-2.0	0.01749596
RC_H84761_s_at	599	H84761	glutathione peroxidase 13p21.3	-2.0	0.000116621
M34338_s_at	683	M34338	spermidine synthase1p36-p22	-2.0	0.008566137
L13698_at	638	L13698	growth arrest-specific 19q21.3-q22.1	-2.0	0.016504513
RC_N75960_at	781	N75960	ESTs	-2.0	0.024082428
D45370_at	491	D45370	adipose specific 210	-2.0	0.034362163
RC_AA401965_at	258	AA401965	tumor suppressor deleted in oral cancer-related 111q13	-2.0	0.011190087
RC_F09315_at	534	F09315	discs, large (Drosophila) homolog 510q23	-2.0	0.020753036
RC_AA025370_at	15	AA025370	KIAA0872 protein	-2.0	0.026565555
RC_H52835_at	579	H52835	phytanoyl-CoA hydroxylase (Refsum disease)10pter-p11.2	-2.0	0.015021251
RC_H99648_s_at	613	H99648	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis5q22-q23	-2.0	0.012115852
RC_AA430074_at	320	AA430074	ESTs	-2.0	0.002355049
RC_AA598939_at	428	AA598939	ESTs	-2.0	0.011383872
AA455001_s_at	368	AA455001	ESTs	-2.0	0.000176199
RC_F09684_at	535	F09684	ESTs	-2.0	0.002741682
D42073_at	490	D42073	reticulocalbin 1, EF-hand calcium binding domain11p13	-2.0	0.012881688
RC_AA598695_at	427	AA598695	ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	-2.0	4.77268E-06
D23662_at	481	D23662	neural precursor cell expressed, developmentally down-regulated 8	-2.0	0.003156141
RC_AA431470_at	323	AA431470	protein kinase (cAMP-dependent, catalytic) inhibitor gamma20q	-2.0	0.038692982
RC_AA399273_at	253	AA399273	ESTs	-2.0	0.029403118
RC_AA142858_at	82	AA142858	ESTs	-2.0	0.00197166

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Table 2 **Normal1-Normal2 vs BPH-Cancer (Up-regulated)** 1669988.1

Affymetrix element	SEQ ID NO:	Genbank ID	Genbank Name	Fold-Change N1-N2 vs Cancer	p-value N1-N2 vs Cancer
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B19q13.3	18.8	0.03580379
RC_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3	16.5	8.98673E-05
RC_Z40715_at	1117	Z40715	Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201)	-2.0	0.017206338
RC_AA490341_s_at	417	AA490341	ESTs	-2.0	0.004570941
RC_N67815_f_at	772	N67815	ESTs, Weakly similar to (defline not available 4680655) [H.sapiens]	-2.0	0.002996692
RC_N53359_at	750	N53359	ESTs	-2.0	0.034916164

TABLE 3 **Normal vs. BPH W/Symptoms (Up-regulated)** 1678621.1

Affymetrix element	SEQ ID NO:	GenBank ID	GenBank Name	Fold-change	t
N40141_at	743	N40141	JM27 protein	17.4	-7.64
rc_N23730_s_at	724	N23730	v-fos FBJ murine osteosarcoma viral oncogene homolog	10.8	-7.54
rc_AA463726_s_at	386	AA463726	JM27 protein	10.0	-6.56
rc_N23352_s_at	723	N23352	proenkephalin	10.0	-4.53
rc_H64493_f_at	590	H64493	immunoglobulin heavy constant gamma 3 (G3m marker)	9.1	-4.36
V01512_rna1_at	993	V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog	9.1	-7.40
rc_H05704_r_at	549	H05704	HCR (a-helix coiled-coil rod homologue)	8.1	-2.79
L49169_at	649	L49169	FBJ murine osteosarcoma viral oncogene homolog B	8.0	-5.81
rc_AA410383_at	277	AA410383	B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)	7.5	-3.95
rc_AA131322_s_at	74	AA131322	tryptase, alpha,tryptase, beta (tryptase II)	7.2	-2.81
R56183_s_at	844	R56183	eukaryotic translation initiation factor 3, subunit 6 (48kD)	6.9	-2.77
rc_AA461300_at	381	AA461300	ESTs	6.9	-7.08
J00231_f_at	617	J00231	immunoglobulin heavy constant gamma 3 (G3m marker)	6.7	-4.62
rc_AA427622_s_at	311	AA427622	collagen, type XIII, alpha 1	6.6	-8.25
rc_T90889_at	927	T90889	ESTs	5.6	-3.72
rc_AA402903_f_at	263	AA402903	immunoglobulin heavy constant gamma 3 (G3m marker)	5.6	-3.61
rc_T23622_at	886	T23622	ESTs	5.5	-5.24
rc_T62857_at	903	T62857	ESTs	5.4	-7.85
rc_AA256268_at	175	AA256268	ESTs	5.3	-6.86
rc_R44714_s_at	837	R44714	ESTs	5.3	-4.83
rc_AA236476_at	154	AA236476	transmembrane protein TENB2,	5.1	-3.13
rc_AA028092_s_at	17	AA028092	transcription factor 21	5.1	-5.24
rc_T90619_f_at	926	T90619	actin, gamma 1	5.0	-2.19
J00123_at	616	J00123	proenkephalin	5.0	-3.96
X52541_at	1064	X52541	early growth response 1	4.9	-5.78
rc_AA620825_at	454	AA620825	CGI-43 protein	4.9	-4.59
rc_AA424530_s_at	304	AA424530	ESTs	4.9	-5.42
rc_AA386386_s_at	246	AA386386	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	4.9	-2.64
U62015_at	978	U62015	cysteine-rich, angiogenic inducer, 61	4.9	-6.24
rc_AA188981_at	112	AA188981	highly expressed in cancer, rich in leucine heptad repeats	4.9	-6.67
rc_H21814_f_at	563	H21814	immunoglobulin lambda locus	4.9	-2.67
M60314_at	692	M60314	bone morphogenetic protein 5	4.7	-10.82
rc_T67053_f_at	909	T67053	immunoglobulin lambda locus	4.7	-2.84
rc_N47686_s_at	744	N47686	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	4.7	-3.27
rc_AA436616_at	335	AA436616	ESTs	4.7	-6.34
rc_H60595_s_at	585	H60595	progesterone binding protein	4.7	-2.66
rc_H88338_at	601	H88338	ESTs	4.7	-7.93
M33653_at	682	M33653	collagen, type XIII, alpha 1	4.6	-8.95
rc_N30198_at	733	N30198	ESTs	4.5	-5.87
D83018_at	513	D83018	nel (chicken)-like 2	4.5	-9.79
rc_Z39904_at	1111	Z39904	ESTs	4.5	-6.27
H61295_s_at	586	H61295	CD4 antigen (p55)	4.4	-4.49
rc_AA281345_f_at	201	AA281345	immediate early protein	4.3	-6.62
rc_T23490_s_at	885	T23490	hypothetical protein FLJ20185	4.2	-5.25
rc_AA279760_at	193	AA279760	DKFZP564M182 protein	4.2	-3.73
rc_R25410_at	814	R25410	ESTs	4.2	-4.69
rc_T03229_f_at	874	T03229	ESTs	4.2	-3.37
rc_R93908_at	865	R93908	ESTs	4.2	-3.39
AA374109_at	241	AA374109	spondin 2, extracellular matrix protein	4.2	-1.97
rc_R45654_at	838	R45654	collagen, type XIII, alpha 1	4.2	-5.69
rc_H86112_f_at	600	H86112	KIAA0471 gene product	4.1	-4.00
rc_AA257093_r_at	178	AA257093	T cell receptor beta locus	4.1	-7.77
rc_AA456147_at	371	AA456147	general transcription factor IIIA	4.1	-6.23

U21128_at	953	U21128	lumican	4.1	-6.15
rc_AA057195_at	47	AA057195	TNF? elastin microfibril interface located protein	4.1	-2.22
M63438_s_at	696	M63438	immunoglobulin kappa variable 1D-8	4.0	-2.53
M57466_s_at	690	M57466	major histocompatibility complex, class II, DP beta 1	4.0	-3.91
rc_AA443923_at	344	AA443923	cat eye syndrome critical region gene 1	4.0	-3.01
rc_N39415_at	742	N39415	DKFZP586P2421 protein	4.0	-5.70
rc_W67225_at	1021	W67225	KIAA0592 protein	4.0	-3.35
M62831_at	695	M62831	immediate early protein	4.0	-6.39
rc_AA404957_at	266	AA404957	matrix Gla protein	4.0	-3.84
rc_F02992_at	526	F02992	ESTs	4.0	-3.65
U69263_at	982	U69263	matrilin 2	3.9	-4.84
rc_AA448625_at	354	AA448625	slit (Drosophila) homolog 3	3.9	-4.13
X57025_at	1066	X57025	insulin-like growth factor 1 (somatomedin C)	3.9	-3.93
AA151544_at	91	AA151544	matrix metalloproteinase 23B	3.8	-5.54
rc_F13763_at	542	F13763	ESTs	3.8	-6.39
rc_AA436655_at	337	AA436655	hypothetical protein FLJ10781	3.8	-5.13
M87789_s_at	704	M87789	immunoglobulin heavy constant gamma 3 (G3m marker)	3.8	-3.93
L44416_at	647	L44416	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD)	3.8	-1.75
U20350_at	951	U20350	chemokine (C-X3-C) receptor 1	3.8	-6.50
rc_AA449749_at	355	AA449749	ESTs	3.8	-4.52
rc_W73790_f_at	1027	W73790	immunoglobulin lambda-like polypeptide 1	3.7	-2.95
rc_AA281145_at	200	AA281145	ESTs	3.7	-1.77
rc_f09748_s_at	536	F09748	ESTs	3.7	-4.12
rc_T64211_at	906	T64211	HNOEL-iso protein	3.7	-5.35
rc_N80152_at	786	N80152	RNA binding motif protein 6	3.7	-2.40
rc_AA436618_at	336	AA436618	microtubule-associated protein 2	3.7	-4.67
T85532_f_at	917	T85532	ESTs	3.7	-1.90
rc_AA398280_at	248	AA398280	ESTs	3.6	-3.11
rc_T23468_at	884	T23468	CGI-119 protein	3.6	-4.67
AA195678_at	117	AA195678	actin binding protein; macrophin (microfilament and actin filament cross-linker protein)	3.6	-3.48
AB002335_at	460	AB002335	KIAA0337 gene product	3.6	-4.21
rc_AA598982_s_at	429	AA598982	KIAA1114 protein,trophinin	3.6	-4.58
J03507_at	621	J03507	complement component 7	3.6	-6.21
J04130_s_at	625	J04130	small inducible cytokine A4 (homologous to mouse Mip-1b)	3.5	-4.76
AA495865_at	421	AA495865	ESTs	3.5	-3.65
HG3543-HT3739_at		HG3543-HT3739	insulin-like growth factor 2 (somatomedin A)	3.5	-4.69
rc_AA599662_s_at	439	AA599662	KIAA0534 protein	3.5	-4.32
rc_AA486072_i_at	410	AA486072	small inducible cytokine A5 (RANTES)	3.5	-3.88
rc_Z39983_s_at	1112	Z39983	KIAA0561 protein	3.5	-5.56
rc_F02333_at	523	F02333	hypothetical protein FLJ20093	3.5	-2.23
rc_AA151210_at	89	AA151210	ESTs	3.5	-4.20
rc_N92239_at	793	N92239	Wnt inhibitory factor-1	3.5	-3.06
rc_AA173223_at	108	AA173223	ESTs	3.5	-5.22
rc_T86148_s_at	919	T86148	pituitary tumor-transforming 1 interacting protein	3.5	-2.15
AA214688_at	129	AA214688	eukaryotic translation initiation factor 4B	3.5	-3.13
rc_AA216589_at	131	AA216589	ESTs	3.5	-4.40
rc_AA446661_at	347	AA446661	hypothetical protein FLJ10970	3.4	-3.69
AA082546_at	54	AA082546	ESTs	3.4	-4.12
rc_W46395_at	1009	W46395	chromobox homolog 6	3.4	-2.41
rc_AA401433_at	257	AA401433	ESTs	3.4	-3.17
D62965_at	502	D62965	ESTs	3.4	-2.07
rc_AA057829_s_at	48	AA057829	growth arrest-specific 6	3.4	-2.00
rc_AA009755_at	6	AA009755	ESTs	3.3	-4.77
AA247204_at	163	AA247204	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	3.3	-2.85
D13628_at	476	D13628	angiopoietin 1	3.3	-4.86
rc_N59866_at	761	N59866	ESTs	3.3	-4.39
rc_AA406371_at	273	AA406371	ESTs	3.3	-4.98
rc_N67876_s_at	773	N67876	insulin-like growth factor 1 (somatomedin C)	3.3	-3.06

M84526_at	703	M84526	D component of complement (adipsin)	3.3	-3.06
rc_AA234095_at	144	AA234095	hypothetical protein FLJ20701	3.3	-3.78
rc_D60074_s_at	498	D60074	cadherin 10 (T2-cadherin)	3.3	-5.05
rc_T49602_s_at	896	T49602	ESTs	3.3	-3.36
rc_n22006_s_at	718	N22006	ESTs	3.3	-3.88
rc_F04112_f_at	530	F04112	ESTs	3.3	-3.26
rc_T64223_s_at	907	T64223	carboxypeptidase A3 (mast cell)	3.3	-2.97
U23946_at	955	U23946	RNA binding motif protein 5	3.2	-3.48
rc_AA358038_at	238	AA358038	SH3-binding domain glutamic acid-rich protein like	3.2	-3.21
rc_AA019433_at	12	AA019433	ESTs	3.2	-3.88
X03689_s_at	1044	X03689	eukaryotic translation elongation factor 1 alpha 1	3.2	-1.91
rc_H17550_at	559	H17550	ESTs	3.2	-2.90
rc_AA047880_at	38	AA047880	prothymosin, alpha (gene sequence 28)	3.2	-5.88
rc_AA084138_at	55	AA084138	ESTs	3.2	-7.93
rc_AA599365_at	434	AA599365	decorin	3.2	-4.42
rc_N91971_f_at	791	N91971	retinol-binding protein 1, cellular	3.2	-4.13
rc_T62873_at	904	T62873	ESTs	3.2	-2.12
rc_N49899_at	746	N49899	ESTs	3.2	-3.73
AA298981_at	226	AA298981	fibulin 5	3.2	-6.06
rc_AA479286_at	403	AA479286	ESTs	3.2	-3.54
J04111_at	624	J04111	v-jun avian sarcoma virus 17 oncogene homolog	3.2	-5.47
rc_AA465491_at	391	AA465491	Mad4 homolog	3.2	-2.75
W28548_at	997	W28548	ESTs	3.2	-3.59
AA308998_at	227	AA308998	endothelial differentiation-related factor 1	3.2	-2.89
rc_AA488432_at	412	AA488432	phosphoserine phosphatase	3.2	-3.48
rc_AA598991_at	430	AA598991	amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)	3.1	-4.51
AA463311_at	384	AA463311	hypothetical protein similar to mouse Fbw5	3.1	-2.57
rc_AA147224_at	85	AA147224	ESTs	3.1	-4.41
rc_AA609504_at	444	AA609504	fibronectin leucine rich transmembrane protein 2	3.1	-3.81
U20734_s_at	952	U20734	jun B proto-oncogene	3.1	-3.37
U06863_at	941	U06863	follistatin-like 1	3.1	-2.48
W51743_at	1011	W51743	ESTs	3.1	-2.95
rc_AA465093_at	389	AA465093	TIA1 cytotoxic granule-associated RNA-binding protein	3.1	-5.34
rc_AA219100_at	132	AA219100	DKFZP586P2421 protein	3.1	-4.09
rc_R42424_at	832	R42424	ESTs	3.1	-3.82
rc_W73038_at	1026	W73038	ESTs	3.1	-2.23
AA091278_at	60	AA091278	hypothetical protein FLJ10793	3.1	-2.75
rc_AA620289_at	451	AA620289	PRO0518 protein	3.1	-2.55
rc_AA149579_at	87	AA149579	prostate cancer associated protein 1	3.1	-2.66
M21121_at	668	M21121	small inducible cytokine A5 (RANTES)	3.1	-4.97
rc_AA427890_at	312	AA427890	ESTs	3.1	-4.32
M34516_r_at	684	M34516	immunoglobulin lambda-like polypeptide 1	3.1	-3.47
rc_AA233347_at	140	AA233347	zinc finger protein 216	3.1	-2.43
rc_W74533_at	1029	W74533	latrophilin	3.1	-3.51
rc_AA029597_at	19	AA029597	bone morphogenetic protein 7 (osteogenic protein 1)	3.1	-3.80
rc_N91887_s_at	790	N91887	thymosin, beta, identified in neuroblastoma cells	3.1	-4.47
rc_AA205724_at	123	AA205724	ESTs	3.0	-6.70
U30521_at	960	U30521	P311 protein	3.0	-6.06
X07109_at	1052	X07109	protein kinase C, beta 1	3.0	-4.90
D82346_at	511	D82346	potassium voltage-gated channel, KQT-like subfamily, member 2	3.0	-3.49
rc_AA478962_at	400	AA478962	ESTs	3.0	-3.35
rc_AA151428_s_at	90	AA151428	matrix metalloproteinase 23A,matrix metalloproteinase 23B	3.0	-2.78
rc_AA130349_at	73	AA130349	ESTs	3.0	-2.01
M18737_rna1_at	661	M18737	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	3.0	-5.90
rc_N91461_at	789	N91461	ESTs	3.0	-3.43
rc_AA045481_at	30	AA045481	ESTs	3.0	-3.70
U91903_at	989	U91903	frizzled-related protein	3.0	-4.73

U19495_s_at	950	U19495	stromal cell-derived factor 1	3.0	-4.38
M33493_s_at	680	M33493	tryptase, alpha,tryptase, beta (tryptase II)	3.0	-3.12
Y12711_at	1103	Y12711	progesterone binding protein	3.0	-2.33
rc_N58172_at	757	N58172	ESTs	3.0	-2.53
M12529_at	655	M12529	apolipoprotein E	3.0	-1.92
rc_AA412505_at	288	AA412505	ESTs	3.0	-3.35
U45955_at	967	U45955	glycoprotein M6B	3.0	-4.09
rc_H56673_at	581	H56673	ESTs	3.0	-4.25
L33799_at	645	L33799	procollagen C-endopeptidase enhancer	3.0	-4.72
rc_Z40186_at	1114	Z40186	ESTs	3.0	-2.22
AA094800_at	64	AA094800	eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)	2.9	-2.56
D21063_at	480	D21063	minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin)	2.9	-5.27
rc_AA412049_at	284	AA412049	ESTs	2.9	-2.63
rc_AA599661_at	438	AA599661	ESTs	2.9	-8.62
L02870_s_at	633	L02870	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive)	2.9	-4.69
rc_AA232266_s_at	138	AA232266	ESTs	2.9	-3.22
L02321_at	631	L02321	glutathione S-transferase M5	2.9	-3.33
rc_AA428325_at	315	AA428325	SEC14 (S. cerevisiae)-like 2	2.9	-3.52
D82534_at	512	D82534	f-box and leucine-rich repeat protein 5	2.9	-2.20
rc_T32113_at	889	T32113	KIAA0657 protein	2.9	-2.47
rc_R10896_at	808	R10896	cytochrome c oxidase subunit VIIa polypeptide 2 like	2.9	-1.99
rc_AA019034_i_at	11	AA019034	ESTs	2.9	-4.40
D28423_at	485	D28423	ESTs	2.9	-2.31
rc_AA609943_at	449	AA609943	ESTs	2.9	-3.86
W69302_at	1023	W69302	ESTs	2.9	-2.68
rc_H01824_f_at	544	H01824	GATA-binding protein 2	2.9	-3.82
rc_T67105_s_at	910	T67105	ESTs	2.9	-5.49
rc_AA426372_s_at	307	AA426372	H1 histone family, member X	2.9	-2.53
rc_T98288_f_at	933	T98288	ESTs	2.9	-2.66
rc_N63047_at	762	N63047	ESTs	2.9	-5.25
U57316_at	974	U57316	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2	2.9	-3.59
rc_AA219304_s_at	133	AA219304	alpha-2-macroglobulin	2.9	-1.76

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TABLE 4 **Normal vs. BPH W/Symptoms Table (Down-regulated)** 1678620.1

Affymetrix element	SEQ ID NO:	GenBank ID	GenBank Name	Fold-change	t
rc_T40895_at	892	T40895	protein tyrosine phosphatase type IVA, member 1	16.5	5.19
rc_N80129_i_at	785	N80129	metallothionein 1L	12.6	3.54
rc_AA460914_at	380	AA460914	ESTs	7.4	4.58
rc_AA234996_s_at	147	AA234996	cytochrome c oxidase subunit VIa polypeptide 2	7.2	4.10
X66141_at	1078	X66141	myosin, light polypeptide 2, regulatory, cardiac, slow	6.6	3.80
AA234634_f_at	145	AA234634	CCAAT/enhancer binding protein (C/EBP), delta	6.2	4.35
rc_AA419011_at	296	AA419011	prostate androgen-regulated transcript 1	6.1	3.87
rc_N94303_at	797	N94303	ESTs	5.8	5.96
M20543_at	666	M20543	actin, alpha 1, skeletal muscle	5.5	3.20
rc_AA085943_s_at	58	AA085943	troponin T1, skeletal, slow	5.5	3.02
X06825_at	1050	X06825	tropomyosin 2 (beta)	5.2	3.35
AB000584_at	459	AB000584	prostate differentiation factor	5.1	3.80
M19309_s_at	665	M19309	troponin T1, skeletal, slow	5.0	3.41
rc_AA040433_at	24	AA040433	DKFZP586N2124 protein	5.0	2.62
rc_N32748_at	736	N32748	ESTs	5.0	3.36
rc_AA227926_at	135	AA227926	ESTs	4.8	5.39
rc_AA457566_at	375	AA457566	ESTs	4.7	4.22
rc_AA026641_s_at	16	AA026641	secretory leukocyte protease inhibitor (antileukoproteinase)	4.6	2.09
rc_AA053424_at	40	AA053424	serine/threonine protein kinase MASK	4.5	4.16
V00594_at	992	V00594	metallothionein 2A	4.5	3.71
rc_R16983_at	811	R16983	ESTs	4.5	3.23
U75272_s_at	984	U75272	progastricsin (pepsinogen C)	4.4	4.57
rc_T94447_s_at	928	T94447	cortic al thymocyte receptor (X. laevis CTX) like	4.4	3.50
U08021_at	942	U08021	nicotinamide N-methyltransferase	4.4	2.41
J03910_rna1_at	622	J03910	metallothionein 1G	4.3	2.79
rc_AA236545_at	156	AA236545	ESTs	4.2	2.41
rc_AA211443_at	127	AA211443	ESTs	4.2	4.49
rc_AA398908_at	251	AA398908	ESTs	4.2	2.64
X57129_at	1067	X57129	H1 histone family, member 2	4.2	3.88
M21665_s_at	670	M21665	myosin, heavy polypeptide 7, cardiac muscle, beta	4.1	3.61
X65614_at	1076	X65614	S100 calcium-binding protein P	4.1	4.03
rc_AA197112_r_at	119	AA197112	putative nuclear protein	4.1	3.07
M99487_at	716	M99487	folate hydrolase (prostate-specific membrane antigen) 1	4.0	2.65
X04201_at	1045	X04201	neurotrophic tyrosine kinase, receptor, type 1	3.9	2.87
X05451_s_at	1046	X05451	ESTs	3.9	3.26
rc_AA435720_i_at	328	AA435720	tubulin, alpha 2	3.9	2.20
rc_N92502_s_at	794	N92502	ESTs	3.8	3.11
L77701_at	651	L77701	COX17 (yeast) homolog, cytochrome c oxidase assembly protein	3.8	3.97
HG2157-HT2227_at		HG2157-HT2227	ESTs	3.8	4.08
X76717_at	1087	X76717	metallothionein 1L	3.8	5.82
HG1067-HT1067_r_at		HG1067-HT1067	ESTs	3.7	3.02
rc_AA599331_at	433	AA599331	CGI-119 protein, uncharacterized bone marrow protein BM039	3.6	4.90
M20642_s_at	667	M20642	ESTs	3.6	3.48
rc_AA055163_at	44	AA055163	calsequestrin 2, cardiac muscle	3.6	3.66
rc_AA127946_at	72	AA127946	DKFZP586B2022 protein	3.6	4.40
rc_AA022886_at	14	AA022886	retinal degeneration B beta	3.6	3.51
rc_AA342337_at	231	AA342337	ESTs	3.5	2.57
X02544_at	1042	X02544	orosomucoid 1	3.5	1.92
rc_T73433_s_at	912	T73433	angiotensinogen	3.5	3.10
M21494_at	669	M21494	creatine kinase, muscle	3.4	2.46
rc_AA488072_s_at	411	AA488072	cardiac ankyrin repeat protein	3.4	2.78

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rc_AA293187_s_at	223	AA293187	B-cell CLL/lymphoma 3	3.4	1.62
rc_AA599522_r_at	437	AA599522	squamous cell carcinoma antigen recognised by T cells	3.4	3.03
rc_AA405488_at	268	AA405488	ESTs	3.4	2.57
rc_AA461453_at	382	AA461453	calcium binding protein Cab45 precursor,	3.4	3.10
rc_AA609006_at	440	AA609006	ESTs	3.4	2.30
rc_N24761_at	725	N24761	TU12B1-TY protein	3.4	3.89
rc_AA432162_at	324	AA432162	DKFZP586B2022 protein	3.4	2.78
X06256_at	1047	X06256	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	3.4	4.51
rc_AA045825_at	33	AA045825	ESTs	3.3	3.90
rc_AA478778_at	399	AA478778	ESTs	3.3	4.37
rc_N80129_f_at	785	N80129	metallothionein 1L	3.2	3.60
rc_AA182030_at	110	AA182030	pyruvate dehydrogenase kinase, isoenzyme 4	3.2	3.72
rc_AA102489_at	67	AA102489	hypothetical protein FLJ10337	3.2	2.20
rc_R46074_at	840	R46074	transforming, acidic coiled-coil containing protein 2	3.2	3.38
rc_AA599522_f_at	437	AA599522	squamous cell carcinoma antigen recognised by T cells	3.2	2.36
rc_AA165313_at	104	AA165313	ESTs	3.2	2.76
rc_AA429636_at	319	AA429636	hexokinase 2	3.2	3.12
rc_R71792_s_at	855	R71792	thrombospondin 1	3.1	2.31
U05861_at	940	U05861	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase),aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	3.1	2.62
rc_AA410311_at	275	AA410311	ESTs	3.1	3.52
rc_AA505136_at	426	AA505136	ESTs	3.1	3.00
rc_T68873_f_at	911	T68873	metallothionein 1L	3.0	3.18
X00371_ma1_at	1041	X00371	myoglobin	3.0	2.18
rc_AA099820_at	65	AA099820	ESTs	3.0	3.08
rc_T90190_s_at	925	T90190	H1 histone family, member 2	3.0	3.48
rc_AA227936_f_at	136	AA227936	parathymosin	3.0	1.76
X90568_at	1092	X90568	titin	3.0	2.83
rc_AA004699_at	1	AA004699	orphan G-protein coupled receptor	3.0	2.23
rc_F03969_at	528	F03969	ESTs	2.9	2.53
X93036_at	1093	X93036	FXYD domain-containing ion transport regulator 3	2.9	2.91
rc_R91484_at	863	R91484	ESTs	2.9	6.43
rc_AA025370_at	15	AA025370	KIAA0872 protein	2.9	2.87
X51441_s_at	1063	X51441	serum amyloid A1	2.9	1.78
X64177_f_at	1075	X64177	metallothionein 1H	2.9	3.36
rc_AA255480_at	173	AA255480	ECSIT	2.9	2.38
rc_AA476944_at	394	AA476944	ESTs	2.8	4.26
U78294_at	985	U78294	arachidonate 15-lipoxygenase, second type	2.8	1.82
rc_AA045487_at	31	AA045487	ESTs	2.8	2.75
rc_N74291_at	779	N74291	ESTs	2.8	1.88
rc_N91973_at	792	N91973	hypothetical protein,three prime repair exonuclease 1	2.8	1.97
D81655_at	510	D81655	ESTs	2.8	1.89
U53225_at	971	U53225	sorting nexin 1	2.8	3.16
rc_H77597_f_at	594	H77597	metallothionein 1H	2.8	2.98
K02215_at	628	K02215	angiotensinogen	2.8	3.05
rc_AA464728_s_at	388	AA464728	ESTs	2.7	3.80
rc_W49708_at	1010	W49708	ESTs	2.7	3.52
rc_AA453435_at	364	AA453435	ESTs	2.7	4.78
rc_D11824_at	474	D11824	ESTs	2.7	3.70
rc_T56281_f_at	902	T56281	RNA helicase-related protein	2.7	2.62
rc_AA182882_at	111	AA182882	titin-cap (telethonin)	2.7	1.85
rc_AA447522_at	349	AA447522	ESTs	2.7	3.27
rc_N26904_at	731	N26904	FK506 binding protein precursor	2.7	3.21
rc_AA131919_at	75	AA131919	putative type II membrane protein	2.7	4.15
rc_R89840_at	862	R89840	ESTs	2.7	2.23

rc_W31470_at	998	W31470	thyroid hormone receptor-associated protein, 95-kD subunit	2.7	2.85
rc_W92207_at	1036	W92207	ESTs	2.7	4.07
U96094_at	990	U96094	sarcolipin	2.7	2.23
rc_W70131_at	1024	W70131	ESTs	2.7	3.64
rc_AA435720_f_at	328	AA435720	tubulin, alpha 2	2.7	1.98
rc_AA284879_at	212	AA284879	ESTs	2.7	1.74
rc_H22453_at	564	H22453	ESTs	2.7	4.20
D14826_s_at	478	D14826	cAMP responsive element modulator	2.6	4.13
rc_N93798_at	796	N93798	protein tyrosine phosphatase type IVA, member 3	2.6	3.12
U41804_at	965	U41804	putative T1/ST2 receptor binding protein	2.6	4.37
rc_W20486_f_at	995	W20486	chromosome 21 open reading frame 56	2.6	2.74
rc_AA055768_at	45	AA055768	CGI-119 protein	2.6	2.13
rc_AA447977_s_at	352	AA447977	ESTs	2.6	3.22
AA380393_at	243	AA380393	SEC7 homolog	2.6	2.29
rc_N29568_at	732	N29568	thyroid hormone receptor-associated protein, 150 kDa subunit	2.6	2.46
rc_AA426374_f_at	308	AA426374	tubulin, alpha 2	2.6	3.20
rc_H94471_at	604	H94471	occludin	2.6	2.19
rc_AA252219_at	169	AA252219	ESTs	2.6	3.83
rc_AA402000_at	259	AA402000	ESTs	2.6	2.29
rc_Z38744_at	1108	Z38744	putative gene product	2.6	4.18
AA045870_at	34	AA045870	ESTs	2.6	2.26
rc_R38678_at	823	R38678	ESTs	2.6	4.16
R39467_f_at	826	R39467	NEU1 protein	2.6	2.79
AA455001_s_at	368	AA455001	CGI-43 protein	2.6	5.34
rc_AA292328_at	221	AA292328	activating transcription factor 5	2.6	2.88
X57348_s_at	1068	X57348	stratifin	2.6	2.48
rc_T95005_s_at	929	T95005	ESTs	2.5	3.30
AA410355_at	276	AA410355	ribosomal protein S6 kinase, 70kD, polypeptide	2.5	2.31
AA036900_at	21	AA036900	ESTs	2.5	2.45
rc_F02204_at	521	F02204	BAI1-associated protein 2	2.5	2.26
U26173_s_at	958	U26173	nuclear factor, interleukin 3 regulated	2.5	3.91
rc_AA477767_at	396	AA477767	ESTs	2.5	3.17
rc_AA504805_s_at	424	AA504805	interferon stimulated gene (20kD)	2.5	3.79
rc_R33627_i_at	818	R33627	ESTs	2.5	1.99
rc_T40995_f_at	893	T40995	alcohol dehydrogenase 3 (class I), gamma polypeptide	2.5	2.15
rc_R00144_at	801	R00144	ESTs	2.5	2.69
U02020_at	936	U02020	pre-B-cell colony-enhancing factor	2.5	4.20
rc_AA287832_at	217	AA287832	ESTs	2.5	3.80
AA429539_f_at	318	AA429539	hypothetical protein	2.5	2.35
rc_H05084_at	547	H05084	GDP-mannose pyrophosphorylase B	2.5	2.23
rc_AA405616_at	271	AA405616	ESTs	2.5	3.33
AA455381_at	370	AA455381	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	2.4	2.60
M13955_at	658	M13955	keratin 7	2.4	2.22
rc_AA180314_at	109	AA180314	ESTs	2.4	2.53
M37984_rna1_at	688	M37984	troponin C, slow	2.4	2.10
M61764_at	694	M61764	tubulin, gamma 1	2.4	3.48
rc_AA150920_at	88	AA150920	KIAA0539 gene product	2.4	4.11
X65965_s_at	1077	X65965	superoxide dismutase 2, mitochondrial	2.4	2.37
X93510_at	1094	X93510	LIM domain protein	2.4	2.39
rc_N48056_s_at	745	N48056	folate hydrolase (prostate-specific membrane antigen) 1	2.4	1.80
rc_N26713_s_at	729	N26713	ESTs	2.4	3.87
rc_AA282247_at	204	AA282247	ESTs	2.4	3.17
rc_D80617_at	508	D80617	KIAA0596 protein	2.4	2.02
rc_F02245_at	522	F02245	monoamine oxidase A	2.4	2.79
rc_R58878_at	847	R58878	ESTs	2.4	2.80
rc_W45531_at	1007	W45531	ESTs	2.4	4.17
L25270_at	644	L25270	SMC (mouse) homolog, X chromosome	2.4	3.26
rc_W88568_at	1035	W88568	glycogenin 2	2.4	1.90

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rc_AA070752_s_at	51	AA070752	insulin receptor substrate 1	2.4	2.87
U24169_at	956	U24169	JTV1 gene,hypothetical protein PRO0992	2.4	3.41
rc_T15423_s_at	878	T15423	2',3'-cyclic nucleotide 3' phosphodiesterase	2.4	1.71
X78706_at	1088	X78706	carnitine acetyltransferase	2.4	3.51
rc_T10695_i_at	876	T10695	enigma (LIM domain protein)	2.4	1.52
rc_AA430388_at	321	AA430388	HSPC160 protein	2.4	5.04
M68519_rna1_at	699	M68519	surfactant, pulmonary-associated protein A1	2.4	3.89
rc_AA421562_at	300	AA421562	anterior gradient 2 (Xenepus laevis) homolog	2.4	1.80
rc_T97243_at	931	T97243	prenyl protein protease RCE1	2.4	2.46
rc_T15409_f_at	877	T15409	ESTs	2.3	3.76
rc_T62918_at	905	T62918	ESTs	2.3	2.59
rc_R15108_at	810	R15108	ESTs	2.3	2.74
AA454908_s_at	366	AA454908	KIAA0144 gene product	2.3	2.77
rc_N64683_at	764	N64683	CGI-119 protein	2.3	2.27
rc_H99035_at	612	H99035	ESTs	2.3	4.34
Y08374_rna1_at	1100	Y08374	chitinase 3-like 1 (cartilage glycoprotein-39)	2.3	2.94
rc_AA236241_at	150	AA236241	ESTs	2.3	1.57
U52969_at	970	U52969	Purkinje cell protein 4	2.3	3.49
rc_R11526_f_at	809	R11526	parathymosin	2.3	1.71
rc_T15850_f_at	880	T15850	ESTs	2.3	2.42
HG2259-HT2348_s_at		HG2259-HT2348	tubulin, alpha 1 (testis specific),tubulin, alpha, ubiquitous	2.3	2.91
rc_H15143_s_at	554	H15143	ortholog of rat pippin	2.3	1.45
rc_AA101767_at	66	AA101767	ESTs	2.3	3.52
rc_AA193197_at	116	AA193197	sarcomeric muscle protein	2.3	1.98
U03688_at	938	U03688	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	2.3	2.97
rc_R37774_at	822	R37774	cytochrome P450 retinoid metabolizing protein	2.3	4.11
rc_H81413_f_at	597	H81413	high-mobility group (nonhistone chromosomal) protein isoforms I and Y	2.3	3.12
X16354_at	1060	X16354	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	2.3	2.54
rc_AA457235_at	373	AA457235	ESTs	2.3	2.25
D13643_at	477	D13643	KIAA0018 gene product	2.3	1.78
rc_N30856_at	734	N30856	solute carrier family 19 (thiamine transporter), member 2	2.3	3.45
M26311_s_at	673	M26311	S100 calcium-binding protein A9 (calgranulin B)	2.3	2.37
rc_Z40556_at	1116	Z40556	CGI-96 protein	2.3	2.39
rc_N79070_at	783	N79070	ESTs	2.3	1.43
Z69881_at	1122	Z69881	ATPase, Ca++ transporting, ubiquitous	2.3	3.87
rc_D60755_s_at	500	D60755	ESTs	2.3	2.30
rc_N94424_at	798	N94424	retinoic acid receptor responder (tazarotene induced) 1	2.2	1.09

Table 5

Up-regulated genes		Down-regulated genes	
Cluster	Fragment Name	Cluster	Fragment Name
1	rc_AA256268_at	1	rc_AA227926_at
1	rc_AA188981_at	1	rc_AA398908_at
1	rc_AA173223_at	1	L77701_at
1	rc_AA216589_at	1	rc_AA599331_at
1	rc_AA234095_at	1	AA455001_s_at
1	rc_H17550_at	3	rc_AA022886_at
1	AA308998_at	3	rc_N24761_at
1	rc_AA488432_at	3	X06256_at
1	rc_AA427890_at	4	HG1067-HT1067_r_at
1	rc_N91887_s_at	4	rc_AA127946_at
1	rc_AA045481_at	4	rc_AA405488_at
3	rc_T23622_at	5	AA234634_f_at
3	rc_T23490_s_at	5	X65614_at
3	rc_AA620289_at	5	rc_T73433_s_at
4	rc_H05704_r_at	5	rc_R91484_at
4	rc_AA436616_at	5	rc_N93798_at
4	rc_AA456147_at	6	rc_N94303_at
4	rc_f09748_s_at, AA495865_at	6	AB000584_at
4	rc_AA598982_s_at	6	rc_AA410311_at
4	HG3543-HT3739_at	6	rc_F02245_at
4	rc_AA609504_at	7	rc_T40895_at
5	rc_AA028092_s_at	7	rc_N80129_i_at, X76717_at, rc_N80129_f_at, rc_T68873_f_at
5	U62015_at	7	rc_N32748_at
5	rc_F13763_at	7	V00594_at
5	rc_AA205724_at	7	J03910_rna1_at
5	U30521_at	7	X57129_at, rc_T90190_s_at
6	X52541_at	7	rc_AA182030_at
6	rc_AA281345_f_at, M62831_at	7	rc_AA505136_at
7	rc_n22006_s_at	7	X64177_f_at, rc_H77597_f_at
7	rc_R42424_at	7	rc_AA101767_at

TABLE 6 BPH vs. Normal and Cancer

1669495 1

Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
AA092215_at	61	AA092215	potassium channel modulatory factor	0.1086431	0.887604969	0.000105867	0.141381127	0.031099165	0.000775399
AA122242_at	70	AA122242	mannose-6-phosphate receptor (cation dependent)	7.49E-05	0.560180168	0.87992066	0.006231736	0.000301953	0.664273011
AA122302_at	71	AA122302		0.430127474	0.003373118	0.068806262	0.000514723	0.328161735	1.48715E-05
AA155958_at	94	AA155958	S164 protein	0.096247016	0.007959573	0.170003368	8.36688E-05	0.782399153	0.000223021
AA236286_at	151	AA236286	fetal Alzheimer antigen	0.052450894	0.034104742	0.076032207	0.000262856	0.875443134	0.000444882
AA248802_at	165	AA248802	DKFZP564A122 protein	0.000230259	0.38257085	0.842458286	0.026030678	0.000947368	0.500601376
AA293544_at	225	AA293544	D component of complement (adipsin)	7.02821E-05	0.203858328	0.178154822	5.9415E-06	0.012632481	0.019226603
AA376468_at	242	AA376468		0.405364589	0.000353844	0.537460601	0.006147013	0.169320077	7.97148E-05
AA410925_at	278	AA410925	transducin-like enhancer of split 1, homolog of Drosophila E(sp1)	0.870505598	1.09859E-05	0.106359333	4.33855E-05	0.168431987	0.003967521
AA461618_s_at	383	AA461618		0.001614433	0.497688178	0.000768417	0.001055794	6.29856E-10	0.031759146
C15965_at	468	C15965		0.000459149	0 350724893	0.919693498	0.000138025	0.000627643	0.416397432
D10537_s_at	472	D10537	myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)	4.11477E-05	0.923679005	4.72641E-05	0.000899706	0.975645863	0.00098994
D25303_at	482	D25303	integrin, alpha 9	0.00061935	0.196221991	0.000846365	0.108182462	0.935105808	0.124782864
D26598_at	483	D26598	proteasome (prosome, macropain) subunit, beta type, 3	0 000121781	0.02105211	8.45942E-05	0.326778603	0.933101073	0.291769938
D31887_at	489	D31887	KIAA0062 protein	0.000123265	0.125782983	0.000676946	0.084742928	0.675822922	0.174766454
D50532_at	492	D50532	macrophage lectin 2 (calcium dependent)	0.013806312	0.034992941	0.07897755	0.981647465	6.26998E-05	0.000487842
D50550_at	493	D50550	lethal giant larvae (Drosophila) homolog 1	3.10455E-05	0.029363545	4.06139E-05	0.169772872	0.953324091	0.186302331
D64154_at	503	D64154	cell membrane glycoprotein, 110000M(r) (surface antigen)	1.68633E-05	0.000696104	5.00873E-05	0.747380424	0.814285971	0.90759386
D84294_at	514	D84294	tetratricopeptide repeat domain 3	8.04076E-06	0.163620727	0.000752223	0.017501269	0.299205599	0.142785528
D86976_at	515	D86976	minor histocompatibility antigen HA-1	3.35538E-06	0.219311742	4.36833E-07	0.007209475	0.701246025	0.002498824
D87258_at	516	D87258	protease, serine, 11 (IGF binding)	9.00737E-05	0.762310231	0.004565624	0.000386998	0.305696637	0.008038934
D87292_at	517	D87292	thiosulfate sulfurtransferase (rhodanese)	0.004418719	0.000188241	0.000878154	0 222741306	0.648642702	0.412420863
D87465_at	518	D87465	KIAA0275 gene product	7.37644E-05	0.826724125	0.000140053	0.000450807	0.882548967	0.000727958
H19969_at	562	H19969		0.005160656	7.47697E-07	6.71287E-07	0.01521142	0.039287107	0.535558762
H61361_s_at	587	H61361	immunoglobulin superfamily containing leucine-rich repeat	4.92249E-05	0.834280925	5.95931E-05	0.001490555	0.966053313	0.001694157
J00277_at	618	J00277	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	0.035655118	0.055426457	0 009927846	0.000332747	0.650555821	6.72893E-05
J04076_at	623	J04076	early growth response 2 (Krox-20 (Drosophila) homolog)	0.034912914	0.473833846	2.46869E-11	0.285997211	1.48067E-05	1 13903E-06
J04605_at	627	J04605	peptidase D	0.000200727	0.006030981	0.000362209	0.648903631	0.885410388	0.742239283
K03204_f_at	630	K03204	proline-rich protein BstNI subfamily 1	0.283795673	0.000798814	0.913648897	0.019814734	0.26284107	0.000926711
L02326_f_at	632	L02326		0.105345943	0.659037818	6.62426E-05	0.076492051	0.02455672	0.000181614
L05500_at	635	L05500	adenylate cyclase 1 (brain)	0.016699778	0.257619651	3.79921E-05	0.002077455	0.101519111	6.32745E-06
L06797_s_at	636	L06797	chemokine (C-X-C motif), receptor 4 (fusin)	0.443118956	0.447152817	1.30523E-06	0.926525008	0.000111977	0.000981046
L08246_at	637	L08246	myeloid cell leukemia sequence 1 (BCL2-related)	0.043208838	0.230033308	4.68128E-10	0.596833839	6.55684E-05	5.57731E-05
L13740_at	639	L13740	nuclear receptor subfamily 4, group A, member 1	0.791312753	0.872331125	8.60985E-05	0.70798804	7.00025E-05	0.001852799
L13852_at	640	L13852	ubiquitin-activating enzyme E1-like	0 000578096	0.646204921	0.003882395	0.000950816	0.599103668	0.004460291
L19437_at	641	L19437	transaldolase 1	0.008021968	0.22883538	0.001388037	0.000773689	0.604482478	0.000135454

TABLE 6 **BPH vs. Normal and Cancer**

1669495 1

Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
L34587_at	646	L34587	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)	0.000178315	0.105125832	7.09176E-05	0.11839964	0.830767426	0.080296411
L44497_at	648	L44497	cyclic AMP phosphoprotein, 19 kD	0 000816364	0.012044336	0.000161685	0.709380948	0.686659704	0.467540879
L76200_at	650	L76200	guanylate kinase 1	0.000841699	0.002396122	0.000888336	0.889388751	0.988638065	0.879528075
M12959_s_at	656	M12959	T cell receptor alpha locus	3.02601E-08	0.817611534	3.24058E-08	1.14437E-05	0.990909384	1.1981E-05
M13560_s_at	657	M13560	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	0.01541788	0 255419127	4.82527E-06	0.001882075	0.041399052	9.73079E-07
M14660_at	659	M14660		1.95092E-06	0.823404837	0.009910008	0.000180501	0.038673415	0.053432817
M16336_s_at	660	M16336	CD2 antigen (p50), sheep red blood cell receptor	0.000908965	0.444045616	0.000106508	0.042888317	0.596564762	0.01280799
M19154_at	663	M19154	transforming growth factor, beta 2	0.021033675	0.886661499	5.38416E-05	0.039706043	0.100571645	0.00047052
M19283_at	664	M19283	actin, gamma 1	0 009680549	0.975542421	1.35524E-05	0.029109597	0.094241798	0.000262549
M21121_s_at	668	M21121	small inducible cytokine A5 (RANTES)	0.00011935	0.82444906	0.028900951	0.000639223	0.114726075	0.042253328
M31776_s_at	677	M31776	natriuretic peptide precursor B	9.53305E-05	0.786764461	0.00132485	0.000453681	0.511730949	0.003376181
M33552_at	681	M33552	lymphocyte-specific protein 1	0.098325681	0.187562681	0.000373789	0.008253387	0.070738695	2.37353E-05
M37766_at	687	M37766	CD48 antigen (B-cell membrane protein)	0.006750544	0.671986725	0.000173892	0.007796504	0.321364096	0.000414775
M54927_at	689	M54927	proteolipid protein (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)	0.0008203	0.071504547	0.000610665	0.292633338	0.938762949	0.26282367
M59465_at	691	M59465	tumor necrosis factor, alpha-induced protein 3	0.905275899	0.300604716	2.40334E-05	0.370512119	3.79139E-05	6.51796E-06
M60459_at	693	M60459	erythropoietin receptor	5 33228E-07	0.001997812	2.00307E-06	0.229150396	0.804556624	0.324369463
M73077_at	701	M73077	glucocorticoid receptor DNA binding factor 1	4.33165E-05	0.026210722	7.3229E-05	0.205361352	0.906734945	0.244557908
M89796_rna1_at	705	M89796	membrane-spanning 4-domains, subfamily A, member 1	3.38097E-07	0 68414038	0.000659504	0.000116527	0.107834095	0.014565483
M94077_at	709	M94077	loricrin	7.86788E-05	0.167396165	8.55841E-06	0.050135902	0 633682729	0.017465235
M94547_at	710	M94547	myosin light chain 2a	0.000922884	0.001567598	0.000142192	0.778547965	0.641162082	0.898495047
M95678_at	712	M95678	phospholipase C, beta 2	2.65752E-06	0.741444839	0.00021566	0.000330645	0.344847831	0.005753116
M96995_s_at	713	M96995	growth factor receptor-bound protein 2	0.000451432	0.370687613	0.000417356	0.039514013	0.984237779	0.037882757
M98447_rna1_at	714	M98447	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	0.101078475	0.000501168	0.49866517	0.047778543	0.027993512	9.36193E-05
N24990_s_at	728	N24990		0.000594989	0.692375474	0.833157714	0.001206749	0.00054518	0.837698657
R08720_at	805	R08720	hypothetical protein FLJ22609	0 384088189	0.004709624	0.405658837	0.000582614	0.970613897	0.000656156
R33301_at	817	R33301		0.263328276	0.008898636	0.324726425	0.000573184	0.899017203	0.000860093
R39394_at	825	R39394	E1B-55kDa-associated protein 5	0.000120098	0.165965093	0 159597216	5.8721E-06	0.020650662	0.012378795
rc_AA004901_at	2	AA004901		0.00013	0.114226367	0 898931127	2.58485E-06	0.000448774	0.104547963
rc_AA005382_s_at	3	AA005382	granzyme K (serine protease, granzyme 3; tryptase II)	4.06793E-05	0.956799991	0.000100487	0.000772831	0.838991074	0.001451838
rc_AA009615_at	5	AA009615		7.69548E-05	0.013016412	0.000583037	0.366115762	0.625611179	0 634185041
rc_AA010358_at	7	AA010358		1.36211E-06	0.550401822	0.139035486	0.000570081	0.001477269	0.511053692
rc_AA017547_r_at	9	AA017547	hypothetical protein FLJ12387 similar to kinesin light chain	0.989540408	0.214430361	0.000274727	0.228713943	0.000584071	2 44522E-05
rc_AA018414_at	10	AA018414		0.556560157	0.000998026	0.519992597	0.000261037	0.958086097	0.000217926
rc_AA022615_at	13	AA022615	RNA binding motif protein 9	0.000158793	0.509341291	0.263342589	0.000159018	0.011670476	0.117665916
rc_AA037828_at	22	AA037828		0 000583981	0.645542969	0.84290982	0.000955558	0.002108779	0.543978545
rc_AA043196_at	26	AA043196	SMC (mouse) homolog, X chromosome	0.008527895	0.000983583	0.000257323	0.328438436	0.331116816	0.90061816

TABLE 6 BPH vs. Normal and Cancer

1669495 1

Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
rc_AA053267_at	39	AA053267	KIAA1023 protein	0 000119181	0.288536772	0.388296579	2.42934E-05	0.004627114	0.082295734
rc_AA053883_at	41	AA053883		4.95718E-05	0.962839667	0.16054889	0.000624096	0.01179586	0.225390364
rc_AA054222_at	42	AA054222		0.39176403	0.002571399	0.102566251	0.000307234	0.461555799	2.09152E-05
rc_AA055081_at	43	AA055081		6 36828E-05	0.206434411	0.797911434	5.59851E-06	5.42681E-05	0.316914958
rc_AA065173_at	49	AA065173	chromosome 5 open reading frame 4	2.52678E-07	0.570857861	0.058275966	0.000180212	0.001970189	0.302526217
rc_AA069913_at	50	AA069913		0.653765843	0.52776555	5.65709E-06	0.815416554	0.000104293	0.00152505
rc_AA071558_at	52	AA071558		0.168309619	0.418677904	0.000189452	0.054446269	0.025471654	0.000103274
rc_AA082041_at	53	AA082041	likely homolog of rat kinase D-interacting substance of 220 kDa; KIAA1250 protein	0.000143369	0.247732655	0.871515758	0.040056839	0.000552895	0.3290855
rc_AA084324_at	56	AA084324		0.000226203	0.056433291	0.000687497	0.216607531	0.780835192	0.321404997
rc_AA085608_at	57	AA085608	KIAA1041 protein	0.029391584	0.03435634	0.041546789	0.000120442	0.894217078	0.000192545
rc_AA114858_at	68	AA114858	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	0.000210292	0.155417252	0.994165585	8.63652E-06	0.000449478	0.170373425
rc_AA132239_at	76	AA132239		0.012168107	5.56988E-05	4.55236E-05	0.074087524	0.136307788	0.631558319
rc_AA132453_at	77	AA132453		0 000489304	0.141814616	8.74406E-05	0.136343527	0.678807616	0.063921338
rc_AA136864_at	81	AA136864	zinc finger protein homologous to Zfp-36 in mouse	0 000224205	0.630168118	4.9041E-05	0.009114985	0.72551107	0.003549498
rc_AA143190_s_at	83	AA143190	CGI-147 protein	5.31694E-05	0.028242427	0.000127165	0.209594394	0.842566905	0.279924929
rc_AA143467_at	84	AA143467	hypothetical protein FLJ20343	1.62361E-06	0.259338862	1.37865E-06	0.003657312	0.975267724	0.003351742
rc_AA149051_at	86	AA149051		4 08493E-05	0.490333235	0.026825837	4.57567E-05	0.07318676	0.012248149
rc_AA152408_at	93	AA152408	KIAA0433 protein	2.97974E-05	0.362537361	0.455914763	1.36986E-05	0.001140199	0.13486533
rc_AA156064_at	95	AA156064		0.275270351	0.000333624	0.875633108	0.011111677	0.23661308	0.000347347
rc_AA158132_at	98	AA158132	nudix (nucleoside diphosphate linked moiety X)-type motif 5	0.004899515	0.643469716	4.65182E-07	0.057915819	0.034659352	0.000177571
rc_AA165116_at	101	AA165116		0.000384885	0.681603266	0.211571862	0.000813512	0.029042963	0.151679697
rc_AA165231_at	102	AA165231		0.002549485	0.173959444	0 254670513	0.000135147	8.0406E-05	0.719982481
rc_AA169837_at	105	AA169837	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase)	0.08971279	0.008766485	0.091371238	8.4903E-05	0.993409911	8.74977E-05
rc_AA172188_at	107	AA172188	protocadherin alpha 5	0.000667976	0.267150381	4.96881E-06	0.077589163	0.269599078	0.006273958
rc_AA189015_at	113	AA189015	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	0.083660421	0.006384313	1.64695E-08	0.237580015	0.000203416	0.037803249
rc_AA192553_at	115	AA192553	uncoupling protein 3 (mitochondrial, proton carrier)	0.10098208	0.00017981	0.933630822	0.02546947	0.102059527	0.000244309
rc_AA196549_at	118	AA196549		0.001049524	0.569766558	0 000482225	0.001065463	0.839463674	0.000559925
rc_AA205072_at	120	AA205072	KIAA0980 protein	0.000335755	0.586934845	0 684865398	0.000455367	0.002552925	0.389985886
rc_AA205460_at	122	AA205460		0.000108573	0.165439416	0.84259483	5.28568E-06	0.000494762	0.134180366
rc_AA205947_at	124	AA205947	HHGP protein	0.000271962	0.552878143	0.70583219	0.000318994	0.001963327	0.376568675
rc_AA207103_at	125	AA207103	amiloride-sensitive cation channel 2, neuronal	2 05331E-05	0.045239142	0.642629872	0.10526525	0.000317921	0.124103707
rc_AA211300_at	126	AA211300	KIAA0627 protein; Drosophila "multiple asters" (Mast)-like homolog 2	0.004445798	0.287777463	0.006200387	0.000703498	0.918638362	0.000971608
rc_AA211835_s_at	128	AA211835	MHC class II transactivator	0.001672055	0 122505424	0.000371358	4.15083E-05	0.692673582	8.76636E-06
rc_AA215379_at	130	AA215379		7.98828E-05	0.366787682	0.194666913	3.33447E-05	0.012005727	0.051632715
rc_AA228020_at	137	AA228020	splicing factor (CC1.3)	0.00047128	0.328754864	0.940819016	0.000119264	0.001167483	0.317270472
rc_AA233545_at	141	AA233545	AD-003 protein	0.004492717	0.655215048	2.53288E-07	0.052976799	0.028149978	0.000113193
rc_AA233854_at	142	AA233854	S-phase kinase-associated protein 2 (p45)	3.79954E-05	0.744241299	0.538817385	0.001845337	0 000884538	0.84309443
rc_AA233935_at	143	AA233935		0 000608235	0.578078963	0.30216801	0.00070772	0.023016587	0.163656536
rc_AA234831_at	146	AA234831	KIAA0788 protein	0.000575081	0.410892837	0.954176902	0.000257285	0.000897188	0.457935122
rc_AA236453_at	152	AA236453		0 036687413	0.061484767	0.023140149	0.000407818	0 863002571	0.000227528
rc_AA236477_at	155	AA236477	KIAA1559 protein	0.000207423	0.453577644	0.288868663	0.000140775	0 011962605	0.1090363
rc_AA236822_at	157	AA236822	KIAA1097 protein	0.008052957	0.439727961	0.000891185	0.003207259	0.52319673	0.000453056

TABLE 6 **BPH vs. Normal and Cancer**

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Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
rc_AA237011_at	158	AA237011	ATP-binding cassette, sub-family F (GCN20), member 1	0.000202964	0.000263744	1.87304E-06	0.678815593	0.318565402	0.645008985
rc_AA237034_at	159	AA237034	golgi SNAP receptor complex member 2	2.31824E-05	0.319635059	3.30639E-08	0.010320292	0.220104139	0.000272212
rc_AA243416_s_at	160	AA243416	hypothetical protein, expressed in osteoblast	0.033376619	4.72108E-05	0 469143753	0.032420785	0.182985166	0.000942701
rc_AA243698_at	161	AA243698	potassium channel modulatory factor	0 06151528	0.302492952	0.000486853	0.010884151	0.124764794	9.91149E-05
rc_AA243763_at	162	AA243763		0.050706904	0.01206437	0.11555761	5.40095E-05	0.71829242	0.000198301
rc_AA253361_at	172	AA253361		0 000564229	0.000110501	0.010769519	0.397832434	0.394174789	0.11120186
rc_AA255966_at	174	AA255966		0.000512371	0.381782918	0.000368364	0.040324542	0.933794518	0.03373143
rc_AA256486_at	177	AA256486	CGI-141 protein	0.053041853	0.519681482	0.000805238	0.025864118	0.179038095	0.000657368
rc_AA258585_at	180	AA258585	cadherin 19, type 2	8.77783E-08	0.008879695	3.84529E-06	0 0526509	0.488129443	0.183610463
rc_AA258595_f_at	181	AA258595	major histocompatibility complex, class II, DQ beta 1	0.056902737	0.411462581	1.12504E-05	0.017626477	0.018278908	8.86477E-06
rc_AA262107_at	183	AA262107		0 051109951	0.028221779	0.046925687	0.000190669	0.972441626	0.000168986
rc_AA262349_at	184	AA262349	hypothetical protein FLJ10628	0 023368538	0.075191389	0.000520191	0.000323092	0.25384504	4.28987E-06
rc_AA262477_at	185	AA262477	ribonuclease HI, large subunit	0.843423091	0.000293418	0.145801246	0.000917609	0.233064808	0.023283635
rc_AA262969_f_at	186	AA262969	px19-like protein	0.000697965	0.002321008	4.86461E-08	0.916139727	0.050019001	0.106622452
rc_AA278757_at	187	AA278757	KIAA1205 protein	0.000807747	0.701913497	0.00019298	0.001603897	0.719959281	0.000521168
rc_AA278887_at	189	AA278887		4.77289E-05	0.000505266	0.002921534	0.966491221	0.300838621	0.386804461
rc_AA279028_at	190	AA279028		0.269683575	0.000110029	0.896242284	0.00515459	0.355782598	0.000309622
rc_AA279774_at	194	AA279774		0.028330552	0.004250917	0 09766388	4.84994E-06	0.610845854	3.70943E-05
rc_AA279821_s_at	195	AA279821		0.01541818	0.057056528	0.036000999	0.00012115	0.75748484	0.000352962
rc_AA280297_at	196	AA280297		0.004904401	0 069649547	0.030554618	4.43102E-05	0.537205763	0.000396218
rc_AA280309_at	197	AA280309		0.027919295	0.048777883	0.042451847	0.000197325	0.872357649	0.000341621
rc_AA280617_at	198	AA280617		0.020747951	0.100016813	0.006218315	0.000457645	0.687853962	0.000114895
rc_AA282739_at	205	AA282739	Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like)	0.006885251	0.224885918	0.001928329	0.000638964	0.705244944	0.000179491
rc_AA283091_at	206	AA283091	KIAA1219 protein	0.000391955	0.950383286	0.000147487	0.003849943	0.812656175	0.001947884
rc_AA283772_at	207	AA283772	replication factor C (activator 1) 5 (36.5kD)	0 472125644	0.004274231	0.126899001	0.00082772	0.443684418	5.94032E-05
rc_AA283774_at	208	AA283774		0.634799287	0.001085136	0.774459677	0.000408559	0.858121118	0.000730937
rc_AA283907_at	209	AA283907	DC12 protein	0.702306606	0.426110345	0.000364953	0.278959611	0.000181185	0.027738884
rc_AA284777_at	211	AA284777		0 00028958	0.613024306	0.843581256	0.0004624	0.001148934	0.515630593
rc_AA286862_at	214	AA286862	WD repeat domain 6	0.006465478	0.770956466	3.90332E-06	0.047019059	0.072475744	0.000368843
rc_AA287107_s_at	215	AA287107	zinc finger protein ZNF140-like protein	0.000557513	0.647966939	0.168481176	0.000931348	0.049075778	0.113081619
rc_AA287870_s_at	218	AA287870	lymphotoxin beta (TNF superfamily, member 3)	0 042868875	0.904123896	4.72641E-06	0.071763173	0.015492602	8.72095E-05
rc_AA291970_at	220	AA291970	lectomedin-2	0.133517759	0.00116479	0.062658963	1.25187E-05	0.731829127	3.02794E-06
rc_AA292533_at	222	AA292533	putative Rab5-interacting protein	8.63268E-05	0.143959708	1.94797E-06	0.062483153	0.429586131	0.010599279
rc_AA342918_at	232	AA342918	hypothetical protein FLJ22313	0.000298568	0.534260232	0.802167146	0.015864864	0.000243847	0.42047475
rc_AA347578_s_at	234	AA347578	tubulin, beta polypeptide	0.056066605	0.067322154	0.053415125	0.000815763	0.984081099	0.000765743
rc_AA348446_at	235	AA348446		0.00081514	0.498461887	0.002492252	0.000590962	0.75904915	0 001541743
rc_AA349417_at	236	AA349417		0.333508877	4.09468E-05	0.860387174	0.001709823	0.452900772	0.000147762
rc_AA370867_at	239	AA370867		0.000438073	0.000509149	0.076534621	0.678852203	0.097859647	0.062063558
rc_AA371520_at	240	AA371520		0 000956188	0.182406672	0.0004497	0.142299266	0.84509761	0.101288353
rc_AA398719_at	249	AA398719	homolog of rat nadrin	0 005171893	0.312848506	0.003453438	0.000980065	0 903295813	0.000667115
rc_AA399101_at	252	AA399101		0 020406213	0.066006562	0.014033951	0.000219359	0.896140692	0.00013891
rc_AA399542_f_at	254	AA399542		0.225479535	0.502403493	5.62157E-05	0.098347881	0.007549959	6.44137E-05
rc_AA400034_at	255	AA400034		0 250995551	0.01453561	0.033099094	0.00095651	0 35107658	3.77436E-05
rc_AA401297_s_at	256	AA401297	symplekin; Huntingtin interacting protein I	0.012585329	0.166831042	0.004370096	0.000663018	0.73639502	0.000215874
rc_AA402468_at	261	AA402468		0.099732216	9.36987E-05	0.673315411	0.017152495	0.245352826	0.000668187
rc_AA402473_at	262	AA402473		0.457960224	0.000426525	0.079152517	6.26915E-05	0.336346183	1.26194E-06
rc_AA405331_at	267	AA405331	golgi autoantigen, golgin subfamily a, 5	0.586184325	0.001885183	0 429082537	0.000584353	0.815182938	0.00026866
rc_AA405533_at	269	AA405533	integral membrane protein 2B	0.000172614	0.497994468	0.082141472	0.000159183	0.055604922	0.0359498
rc_AA405902_at	272	AA405902		0.086820061	0.039035914	0.014052865	0.000655228	0.480598833	5.66656E-05
rc_AA410954_at	279	AA410954		1.16178E-05	1.50623E-06	1.03048E-05	0.330330235	0.980294091	0.341205824
rc_AA411897_at	281	AA411897		0.508186682	0.001994491	0.445499823	0.00043102	0.923458644	0.000312647

TABLE 6 BPH vs. Normal and Cancer

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Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
rc_AA412267_at	286	AA412267		0.164103629	3.89169E-07	0.756068057	1.61111E-09	0.10637429	3.90003E-06
rc_AA412443_at	287	AA412443		0.364026646	0.005904843	0.355261504	0.000673161	0.987349969	0.000639721
rc_AA417011_at	292	AA417011		0.97881335	0.000103601	0.347607058	0.000209225	0.359543109	6.44615E-06
rc_AA417348_at	293	AA417348		0.011726682	0.000513628	0.000733098	0.214868351	0.416407972	0.597824364
rc_AA417915_at	294	AA417915		0.00031475	0.724609869	0.33434685	0.000849216	0.012345648	0.253561808
rc_AA418557_at	295	AA418557		0 228039568	0.580130356	0.000535144	0.124915173	0.032252409	0.000643742
rc_AA421131_at	298	AA421131		0.000944552	0.385647564	0.015545606	0.00033745	0.400009139	0.00441922
rc_AA421133_at	299	AA421133	erythrocyte transmembrane protein	0.048370115	0.776945443	3.5594E-06	0.170573072	0.011573179	0.000337276
rc_AA424037_s_at	301	AA424037		0.004243716	0.739593135	2.30322E-05	0.006963992	0.192467998	0.000122214
rc_AA424245_at	302	AA424245		0.000912649	0.241386195	0 000606875	0.10233451	0.915105608	0.08414343
rc_AA424515_at	303	AA424515		0.001461647	0.327161944	0.557700471	0.000331758	0.000350136	0.650111174
rc_AA425325_at	305	AA425325		0.000137613	0.761000474	0.006888125	0.000531496	0.292230161	0.011066086
rc_AA425354_at	306	AA425354		1.135E-05	0.848812392	4 31696E-05	0.000125249	0.776028887	0.000335665
rc_AA426438_at	309	AA426438	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	0.086215951	0.051460629	0.077775438	0.000971113	0.963651921	0.000841613
rc_AA426454_s_at	310	AA426454	imidazoline receptor candidate	4.93792E-06	0.168883843	0.000430545	0.013194044	0.320673843	0.1079437
rc_AA427944_at	313	AA427944		0.016580683	2 63482E-05	0.961128446	0.040898728	0.020386125	4.53083E-05
rc_AA428243_at	314	AA428243	integrin beta 4 binding protein	0.000258966	0.030169371	0.000115376	0.338639919	0.847641147	0.260434676
rc_AA428460_at	316	AA428460		0.369406205	2.86818E-05	0.170103625	1.87552E-06	0.031318989	0 00400089
rc_AA429398_s_at	317	AA429398		0.042509423	0.318204908	0.000808205	0.00812556	0.209966492	0.000179435
rc_AA430738_at	322	AA430738	hypothetical protein FLJ22693	2.4223E-05	0.512347676	0.057495876	3.43792E-05	0.027579258	0.027106503
rc_AA433922_at	326	AA433922	NRAS-related gene	0 000129534	0.750927276	0.024589837	0.000483913	0.13400345	0.029612486
rc_AA435753_at	329	AA435753		0.167368191	0 01678153	0.00563702	0.000567982	0.188083313	4.20658E-06
rc_AA435852_at	331	AA435852	hypothetical protein	0 000178813	0.813799408	0.130706548	0.000825341	0.033909282	0.137866512
rc_AA436244_at	332	AA436244		0.000347902	0.773066458	0.838936155	0.006955308	0 000335763	0.655473596
rc_AA436489_at	333	AA436489	dual specificity phosphatase 10	0.089585972	0.000336423	0.53802583	0.042116461	0.028187175	7.58265E-05
rc_AA436548_at	334	AA436548		4.79946E-05	0.79712195	0.073989554	0.000284052	0.03065051	0.082990101
rc_AA436823_at	338	AA436823		3 43729E-06	0.007238466	0.000134014	0.199586541	0.434475995	0.550333062
rc_AA436841_at	339	AA436841	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	0 000757034	0.109130693	3.14861E-05	0.206545207	0.451070087	0.054341855
rc_AA437226_s_at	341	AA437226	interleukin 10 receptor, alpha	0.030634205	0.394007384	3.12463E-06	0.008853685	0 017676075	2.623E-06
rc_AA442830_at	342	AA442830		0.277387057	0.000957882	0.739163222	4.56542E-05	0.474861158	0.000560401
rc_AA446899_at	348	AA446899	mannosidase, alpha, class 1B, member 1	4.08376E-08	0.474845978	8.66417E-09	0.000104871	0.799444331	4.09828E-05
rc_AA448228_at	353	AA448228	HSPC142 protein	0.489815716	0.427628808	0.00011718	0.181303904	1.63664E-05	0.014570459
rc_AA450073_s_at	357	AA450073	paired mesoderm homeo box 1	0.070060208	0.424331633	0.00057893	0.02291416	0 12207024	0.000282414
rc_AA450373_at	361	AA450373		0.19184076	0.000421707	3.75092E-05	0.021344923	0.007526828	0.966348045
rc_AA454016_at	365	AA454016		0.74223808	0.000765848	0.794392558	0.003084476	0.575990681	0.000561238
rc_AA454928_at	367	AA454928	phosphorylase kinase, beta	0.042150436	0.023733581	0.157838834	0.000111797	0.556629171	0.000814363
rc_AA457148_at	372	AA457148		0 770822781	0.643699605	7.37551E-05	0.492232725	0.000493842	0.000182201
rc_AA457407_at	374	AA457407	transmembrane protease, serine 2	0.322389783	0.009487182	0.088848624	0.000914536	0.499415786	9.30818E-05
rc_AA457675_at	376	AA457675		0.000470812	0.007879992	0.000974653	0.721378015	0.850190113	0.848554875
rc_AA459272_at	377	AA459272		8.59013E-05	0.738589634	0.711426345	0.003207799	0.00073865	0.989771621
rc_AA460377_at	378	AA460377	beta-catenin-interacting protein ICAT	0.015059101	0.036482503	0.009644184	5.52729E-05	0.881315511	3.13984E-05
rc_AA464598_at	387	AA464598	KIAA1389 protein	0.000373603	0.650628457	0.000200085	0.000684765	0.878718031	0.000416438
rc_AA469954_at	392	AA469954		0.239197445	0.004848961	0.288136551	0.000228067	0.913292289	0.000330413
rc_AA476594_i_at	393	AA476594	Arg/Abl-interacting protein ArgBP2	0.358342961	0.881892103	0.000846963	0.534258655	5.41111E-05	0.003508506
rc_AA477119_at	395	AA477119		0.155425839	0.46185093	0.00021398	0.058896186	0.030447512	0.000152407
rc_AA477833_at	397	AA477833	translocase of inner mitochondrial membrane 44 (yeast) homolog	0.019542745	0.5471713	3.40147E-05	0.011694366	0.085999006	5.64814E-05
rc_AA478615_s_at	398	AA478615	H1 histone family, member X	0.640957846	0.0022057	0.208838599	0.000871626	0.453348417	6.70146E-05
rc_AA478996_at	401	AA478996		0.680984202	0.000380025	0.977809564	0.000172484	0.677109345	0.000696316
rc_AA481057_f_at	404	AA481057		0.029606002	0.060557911	0.05307758	0.000302603	0.819130316	0.000643675

TABLE 6 BPH vs. Normal and Cancer

1669495 1

Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
rc_aa482107_s_at	406	AA482107		0.412141577	0.217724563	0.000197553	0.061952573	1.63874E-05	0.055779976
rc_AA482559_at	407	AA482559	RPA-binding trans-activator	0.010341566	0.960678267	3.22844E-05	0.02919031	0.130837801	0.000454944
rc_AA485243_at	408	AA485243	leptin receptor	3 17405E-05	0.744743793	0.400224468	0.00016024	0.001638049	0.311183055
rc_AA488658_at	413	AA488658	hypothetical protein	0.000418682	0.365249562	0.186392502	0.000141589	0.036308821	0.048918937
rc_AA488849_at	414	AA488849	nucleotide binding protein 2 (E.coli MinD like)	0.17603882	0.323192094	0.000687853	0.037989302	0.052798072	0.000161003
rc_AA489637_at	415	AA489637		0.003960452	0.871859148	0.000107388	0.010699848	0.346672042	0.000730896
rc_AA490120_at	416	AA490120		0.082001486	0.454413511	0 000859271	0.030324764	0.130537834	0.000479561
rc_AA490520_at	418	AA490520		0.00063489	0.471991068	0.445872157	0.000410063	0.011810787	0.185068096
rc_AA490999_at	420	AA490999		0.001846648	0.670951196	0.000150658	0.002708195	0.521238606	0.000368557
rc_AA504255_at	423	AA504255	ataxia telangiectasia and Rad3 related	0.007747725	1.58087E-05	0.446946913	0.053347131	0.001163384	1.74835E-06
rc_AA505022_at	425	AA505022		0.250524892	0.000259519	0.084574205	7.98938E-06	0.584980634	7.63588E-07
rc_AA599376_at	435	AA599376		0.015748126	0.140670046	0.009272938	0.000615583	0.859099543	0.000343134
rc_AA599443_f_at	436	AA599443	hypothetical protein FLJ10595	0.379179145	0.00382066	0.40828628	0.000446702	0.960279666	0.000525999
rc_AA609657_at	446	AA609657		7 04465E-05	0.091053447	0.00093271	0.092251403	0.5283101	0.25823308
rc_AA609848_at	447	AA609848		0.042723584	0.092999102	0.036171711	0.000967007	0.948118344	0.000787862
rc_AA609869_at	448	AA609869	hypothetical protein FLJ13222	4.47677E-05	0.00053907	2.12675E-07	0.943295205	0.293840522	0.321292026
rc_AA610070_at	450	AA610070	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	0.000126016	0.058243496	0 558814317	0.170494931	2.76548E-05	0.021111632
rc_AA620806_at	453	AA620806	ASB-3 protein	4.7861E-06	0.710135071	0.298838834	0.000563366	0.000797621	0.611912234
rc_AA621325_at	455	AA621325	HNK-1 sulfotransferase	0.000848661	0 346193012	0.004864951	0.000232221	0.621405553	0.001162331
rc_C14898_at	467	C14898		0.000226586	0 885711705	6.82551E-05	0.003389818	0.77964221	0.001496457
rc_C20547_at	469	C20547		0.068260402	0.000952953	0.812550962	2.71206E-06	0.132387942	0.000746928
rc_C20658_at	470	C20658	cisplatin resistance-associated overexpressed protein	0.000322792	0.311886375	0.000285103	7.37384E-05	0.975640568	6.58868E-05
rc_D11789_f_at	473	D11789		0.21798848	0.000243771	0.79113972	0.012426673	0.155631425	0.000180292
rc_D11961_at	475	D11961	hypothetical protein FLJ21343	0.066999427	0.031322113	0.050959636	0.000327468	0.909256528	0.000222056
rc_D20085_at	479	D20085		0.533566658	0.000441315	0.321182892	0.004260671	0.125585439	2.65015E-05
rc_D52692_s_at	497	D52692	Ca2+-dependent activator protein for secretion	1 02115E-06	0.807110908	1.27404E-05	0.000127062	0.619779281	0.000681487
rc_D60272_i_at	499	D60272		0.000665091	0.000166097	0.000151004	0.431868883	0.714339713	0.641956827
rc_D80298_f_at	507	D80298		0.045427886	0.000323207	0 958861584	0.073418502	0.064448036	0.000644976
rc_D80738_f_at	509	D80738		0.190797369	0.00173762	0.245104642	4.17807E-05	0.889912758	7.00818E-05
rc_F01684_at	519	F01684		0.420181016	0.000494834	0.488322276	5.87948E-05	0.914533384	8.72831E-05
rc_F02739_at	525	F02739		5.54856E-05	0.053527575	0.000291424	0.133799091	0.698411971	0.246269511
rc_F04019_at	529	F04019		0.000166861	0 000950517	0.555841593	0.965823573	0.00259065	0.007252422
rc_F10193_at	539	F10193	chromosome 21 open reading frame 39	1.30777E-05	0.948962688	0.020624022	0.000363518	0.05248761	0.062247376
rc_F10323_f_at	540	F10323	retinoblastoma-like 2 (p130)	0.000650946	0.502771636	0.015425251	0.000500148	0.348990394	0.007831047
rc_F10980_at	541	F10980		8.9375E-05	0.653407439	0.012465868	0.000223205	0.178217348	0.012058063
rc_H01068_at	543	H01068		0.86517363	0.000569676	0.466764828	0.001528575	0.394499429	9.00281E-05
rc_H09077_at	551	H09077		3 06359E-05	1.2292E-05	0.021919052	0.46401342	0.07497746	0.021793621
rc_H11463_at	552	H11463	inhibitor of growth family, member 3	0.00061851	0.000440258	0.000113152	0.597222623	0.678354487	0.869200328
rc_H14810_s_at	553	H14810	popeye protein 3	1 36532E-05	0.832182578	0 004057496	0.000637115	0.161519166	0.028710637
rc_H18099_at	560	H18099		0.247088588	0.003400663	0.301565366	0.000158641	0.90607919	0.000239103
rc_H23407_s_at	565	H23407	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1	0.000753122	0.112093793	2 71462E-05	0.201584279	0.432877141	0.049424886
rc_H23520_at	566	H23520		0.611355729	0 000871266	0.849483973	0.000293132	0.507906287	0.002361124
rc_H38418_at	570	H38418		0.185134143	0.065592241	0.008782561	0.50515013	0.000181804	7.8388E-05
rc_H38995_f_at	571	H38995	KIAA0471 gene product	0.009631356	0.97045862	5.86902E-05	0.028554385	0.175136692	0.000728104
rc_H45265_at	574	H45265	ATP-binding cassette, sub-family A (ABC1), member 7	0.000152193	4.19671E-07	0 003258301	0.08727525	0.422648726	0.015812939
rc_H48263_at	575	H48263		0.185258234	0.007096561	0.191295818	0.00022522	0.986389253	0.000238835
rc_H48475_at	576	H48475	ribosomal protein L37a	0 227463546	0.00062116	0.579381783	1.76941E-05	0.535824365	0.000177441
rc_H58781_at	582	H58781		0.042650671	0.000369904	0.497627082	0.082860732	0.010272658	6.73936E-05
rc_H59141_at	584	H59141	hypothetical protein	0.001248184	4.64747E-07	0.066732688	0.031003204	0.185961631	0.000909745
rc_H63994_at	588	H63994		0.042052556	0.003078049	0.051932289	5.75286E-06	0.93248223	8.15902E-06
rc_H64411_at	589	H64411	KIAA0618 gene product	0.01802462	0.070417345	0.012928934	0.000210449	0.908905166	0.000140956

TABLE 6 BPH vs. Normal and Cancer

1669495 1

Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
rc_H77531_s_at	593	H77531	HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A	0.000791123	0.49434307	0 184056577	0.00056294	0.054421223	0.078090378
rc_H97868_at	608	H97868		0.322057918	0.489184724	0.000285548	0.136645099	0.012333089	0.000230315
rc_H97889_at	609	H97889		0.158642014	0.00916284	0.299358664	0.000236375	0 724266848	0.00075937
rc_H98676_at	610	H98676		0.127756769	0.002896791	0.262913685	3.64577E-05	0.701889069	0.000148754
rc_N20967_at	717	N20967		9.92879E-05	0.817666422	3.00688E-05	0.000539948	0.790070901	0.000221099
rc_N22115_s_at	720	N22115	KIAA0447 gene product	5 18274E-07	0.014513808	3.98659E-05	0.067547386	0.387363889	0.284673955
rc_N22297_f_at	721	N22297		0.054494667	0.052949003	0.08027668	0.000541487	0.869037035	0.000917296
rc_N32521_at	735	N32521	hypothetical protein FLJ11085	0 547891484	0.041933612	0.000238523	0.014113039	0.003549591	5.39907E-07
rc_N34517_s_at	738	N34517	integrin, alpha 7	0.005879801	0.196182153	0.004385481	0.00040993	0.928485921	0.000303466
rc_N38882_at	741	N38882		0.014629787	0.005666897	0.251351421	0.530957263	0.000663242	0.000303436
rc_N51579_at	748	N51579	transporter-like protein	0.44766874	6.17952E-05	0.962144968	0.001295779	0.499475206	0.000139415
rc_N54053_at	752	N54053	secreted phosphoprotein 2, 24kD	0 116492665	0.015273471	0.039361645	0.00027615	0.641546757	5.23218E-05
rc_N54845_at	753	N54845		0.000443555	0.073889565	0.000793416	0.227981278	0.881125278	0.282635582
rc_N55085_at	754	N55085		0.220208071	0.876075911	0.000843717	0.384166413	1.49242E-05	0.003419797
rc_N59862_at	760	N59862		0.462122243	0.001300248	0.278791676	0.000214232	0.741521525	6.58223E-05
rc_N66001_at	765	N66001	mouse double minute 4, human homolog of; p53-binding protein	0 269409972	0.001627722	0.449591713	7.93964E-05	0.741058833	0.000255792
rc_N66053_f_at	766	N66053	butyrophilin, subfamily 3, member A1	0.000767668	0.638609685	0.000120387	0.018876455	0.648066184	0.005990603
rc_N67108_at	769	N67108		2.22447E-05	0.94547199	0.335823565	0.000534028	0.00186846	0.462281008
rc_N67324_at	770	N67324		0.061297249	0.015332682	0.029486337	0.000101757	0.771895611	3.46367E-05
rc_N67899_at	774	N67899		8.19817E-05	0.845939057	0 027139019	0.000532728	0.100944503	0.04285656
rc_N80693_at	787	N80693		0 798568519	0.000819546	0.654401168	0.002677747	0.504907369	0.000334108
rc_N89827_at	788	N89827	RALBP1 associated Eps domain containing 2	0.129696038	0.000403735	8.58239E-05	0.032513633	0.022112053	0.895818166
rc_N93495_at	795	N93495	uncharacterized hematopoietic stem/progenitor cells protein MDS033	0.082365924	0 047090947	0.00063645	0.000799522	0.111310122	2.03892E-06
rc_R00440_at	802	R00440	ancient conserved domain protein 4	0.538637852	6.90248E-05	0.927092838	0.000926675	0.619532275	0.000178704
rc_R17000_s_at	812	R17000	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	0.000151792	0.075089669	0.000101925	0.149353698	0.926045731	0.12770179
rc_R25116_at	813	R25116		0.0420832	0.03125809	0.026701279	0.000169518	0 862052816	9.11635E-05
rc_R40030_at	827	R40030	hypothetical protein FLJ20047	0.567472456	0.000280009	0.804462147	0.002571098	0.436977215	0.000218515
rc_R41798_s_at	829	R41798	KIAA1374 protein	0.000373432	0.706910506	0.012448736	0.000894251	0.315054178	0.014659398
rc_R42336_s_at	831	R42336		0.70873782	2.16988E-05	0.77916386	0 000163747	0.929588049	0.000119701
rc_R42525_at	833	R42525		0.050001405	0.071849508	0.013930003	0.000778775	0.635857474	0.000159677
rc_R56216_at	845	R56216		0.000821825	0.352494161	0.151440792	0.0002362	0.069860079	0.036903476
rc_R66690_at	851	R66690		0.548034357	0.001498849	0.392082801	0.000384981	0.808745096	0.000168251
rc_R70212_s_at	853	R70212	CD79A antigen (immunoglobulin-associated alpha)	0.001627385	0.92358255	1.96242E-05	0.011419498	0.28878538	0.000540241
rc_R82942_s_at	856	R82942		4.27278E-06	0.038346252	9 40527E-05	0.06641734	0.511382181	0.207797821
rc_R84968_at	858	R84968		0.029165843	9.17654E-05	0.74623486	0.052010697	0.078018241	0.0004854
rc_R89291_at	861	R89291		0.000287625	0.129809655	0.120359785	7.72734E-06	0.049234398	0.005999323
rc_R92737_at	864	R92737	aquaporin 3	0.045317535	0.54600908	0.000762777	0.024731156	0.195577177	0.000722979
rc_T15530_at	879	T15530		0.039751248	0.193908111	0.000219396	0.003085344	0.119916961	1.53896E-05
rc_T16556_at	882	T16556		0.547027876	0.000735355	0.131501406	0.006096912	0.045271057	6.8433E-06
rc_T49291_s_at	895	T49291	lymphocyte-specific protein 1	0.023580272	0.159004442	0.000765019	0.00120856	0.296144015	3.27932E-05
rc_T50387_at	897	T50387		0.685476265	0.000770227	0.324729565	0.003799426	0.187347142	5.10594E-05
rc_T53404_at	898	T53404	hypothetical protein from clone 643	0.47780256	0.003673041	0.259379562	0.000720609	0.69168737	0.000191916
rc_T54613_at	900	T54613		5.52684E-05	0.022747185	0.000284729	0.24335011	0.701984774	0.40594297
rc_T54617_at	901	T54617		0.857947447	4.07249E-05	0.397904433	0.000148584	0.527265593	0.001199664
rc_T65802_at	908	T65802		0.012663512	0.532196596	0.000313482	0.007483397	0.291974796	0.000319721
rc_T79868_f_at	915	T79868	hypothetical protein 384D8_6	0.071499128	0.033264086	0.074047238	0.000392669	0.987909984	0.000412941
rc_T82292_s_at	916	T82292	protease, serine, 11 (IGF binding)	0 000399556	0.678142361	0.051597503	0.000824339	0.130506724	0.043561586
rc_T86121_at	918	T86121		0.013631945	0.898945913	2.7658E-06	0.029665506	0.035142628	5.76483E-05
rc_T87533_at	920	T87533		0.989160192	0.000472522	0.640089183	0.000751611	0.648053004	0.002981136

TABLE 6 **BPH vs. Normal and Cancer**

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Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs. BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs. Cancer	BPHNoS vs. Cancer
rc_T90038_f_at	924	T90038	butyrophilin, subfamily 3, member A2,butyrophilin, subfamily 3, member A3	4 93914E-06	0.243601757	8.38948E-05	0.007362582	0.547300658	0.031384668
rc_T99373_at	934	T99373		0.026021837	3.07604E-06	0.711043501	0.008523742	0.078371167	2.98773E-05
rc_W37384_i_at	1001	W37384	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	0.000625839	0.217732697	0.000147234	0.096608548	0.7216482	0.048383963
rc_W42483_at	1003	W42483	hypothetical protein similar to mouse Dnajl1	2.97466E-05	0.676684762	0.031770051	0.000106724	0.05435082	0.028721568
rc_W44558_s_at	1005	W44558	adaptor-related protein complex 1, sigma 1 subunit	0.079864992	0.042988764	0.034848175	0.000669599	0.73367308	0.000215475
rc_W60649_at	1019	W60649		0.023339325	0.129224665	0.006757142	0.000824018	0.675851904	0.000206179
rc_W80509_s_at	1032	W80509	death associated transcription factor 1	0 000271744	0.148881601	0.000426903	0.10048575	0 910884693	0.122505852
rc_W86660_at	1034	W86660		0.150249394	6.18841E-06	0.557722374	0.001658036	0.418699422	0.000115844
rc_W93396_at	1038	W93396		0.000180228	0.540603359	0.319667744	0.00021213	0.009081674	0 156804025
rc_Z38551_s_at	1107	Z38551	hypothetical protein FLJ10210	0.007617909	0.125060522	0.00394587	0.000220695	0.839190935	0.000107925
rc_Z39874_at	1110	Z39874		0.018342738	0.000251552	0.969844211	0.120049181	0.022998914	0.000387407
rc_Z40012_f_at	1113	Z40012	NCK-associated protein 1	0 038639336	0.043854062	0.05138364	0.000255085	0.909554475	0.000374451
rc_Z40332_at	1115	Z40332	vesicle docking protein p115	0.028012659	0.10943539	0.012529791	0.000762549	0.7761268	0.000299824
rc_Z41763_at	1120	Z41763		6.03127E-05	0.82776366	0.002670862	0.00038983	0.338788944	0.006770727
S75463_at	871	S75463	Tu translation elongation factor, mitochondrial	0.000271911	0.000533911	0.00172916	0.765671272	0.63019533	0.471338415
S77154_s_at	872	S77154	nuclear receptor subfamily 4, group A, member 2	0.720602576	0.932154297	5.84424E-05	0.829150677	0.000513773	0.001105408
T40327_s_at	891	T40327	electron-transferring-flavoprotein dehydrogenase	7.27596E-06	0.215221988	0.819260055	0.011040692	7.74754E-06	0.167330005
T89243_s_at	922	T89243	KIAA1243 protein	0.00081408	0.517949226	0.114764867	0.000657245	0.092965856	0.053186849
U00672_at	935	U00672	interleukin 10 receptor, alpha	0.000287943	0.609290849	1.66617E-06	0.011540026	0.269359727	0.000474683
U03272_at	937	U03272	fibrillin 2 (congenital contractural arachnodactyly)	0.000310928	0.332521737	0.209649826	8.44451E-05	0.025692948	0.04828388
U04811_at	939	U04811	trophinin	1.5625E-05	0 755433375	0.054905474	0.000984445	0.022792101	0.194301082
U04811_at	939	U04811	trophinin	2.20509E-06	0.327834193	0.000136465	0.002712738	0.383208442	0.025499623
U09366_at	943	U09366	zinc finger protein 133 (clone pHZ-13)	0.000213171	0.5068558	0.610825511	0.000200267	0.002444941	0.288631384
U11861_at	945	U11861	maternal G10 transcript	0.000482828	0.00167301	9.90184E-05	0.90794872	0.702310162	0.826191525
U12775_at	946	U12775	agouti (mouse)-signaling protein	0.000271316	0.000844452	0.000473875	0.859392382	0.889729458	0.765131751
U13220_at	947	U13220	forkhead box F2	0.000592743	0.851887641	3.88357E-05	0.007392289	0.519237	0.001178975
U13991_at	948	U13991	TATA box binding protein (TBP)-associated factor, RNA polymerase II, H, 30kD	1 45014E-06	0.006140037	1.01255E-06	0.168790439	0.946149483	0.151190281
U15932_at	949	U15932	dual specificity phosphatase 5	0.877505283	0.806495835	1.85723E-05	0.914714787	2.57739E-05	0.000146058
U23852_s_at	954	U23852	lymphocyte-specific protein tyrosine kinase	0 015926444	0.891018698	9.08522E-05	0.032567274	0.153847965	0.000703723
U25265_at	957	U25265	mitogen-activated protein kinase kinase 5	8.86395E-06	0.005417963	5.93432E-05	0.305372601	0.684875389	0.503461673
U26174_at	959	U26174	granzyme K (serine protease, granzyme 3, tryptase II)	3.92686E-05	0.206902143	0.000598254	0.027205202	0.519267093	0.10031708
U32674_s_at	962	U32674	G protein-coupled receptor 9	0.003147245	0.1818672	0.076391484	0.000184255	7.37649E-06	0.847933992
U40372_at	963	U40372	phosphodiesterase 1C, calmodulin-dependent (70kD)	0.284766484	1.17113E-05	0.46702597	0.000897191	0.745348724	0.000311221
U43527_at	966	U43527	KiSS-1 metastasis-suppressor	0 068750933	0.878566298	0.000141006	0.096679594	0.059509384	0.000920023
U46006_s_at	968	U46006	cysteine and glycine-rich protein 2	0.000581958	0.677096089	0.000421368	0.013813896	0.93464395	0.011277242

TABLE 6 **BPH vs. Normal and Cancer**

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Affymetrix Fragment Name	SEQ ID NO:	GenBank ID	GenBank Name	P- Values Normal vs. BPHWS	Normal vs BPHNoS	Normal vs. Cancer	BPHWS vs. BPHNoS	BPHWS vs Cancer	BPHNoS vs. Cancer
U52112_rna1_at	969	U52112	L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1)	0.012256648	0.603209864	0.000361314	0.009782964	0.313616052	0.000525936
U55209_at	973	U55209	myosin VIIA (Usher syndrome 1B (autosomal recessive, severe))	0.026307797	0.000534284	5.50778E-05	0.139252083	0.085728294	0.977237559
U57623_s_at	975	U57623	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	0.000249597	0.006076702	2.31411E-07	0.680669423	0.152138423	0.095412354
U58522_at	976	U58522	huntingtin interacting protein 2	0.950874668	0.000404266	0.026015373	0.000816174	0.04004298	0.12201215
U66075_at	980	U66075	GATA-binding protein 6	0.000177786	0.094949773	5.41966E-05	0.129840147	0.784613111	0.079354568
U66615_at	981	U66615	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	0.00427057	0.860602352	0.000125812	0.01088834	0.353965999	0.000781605
U89922_s_at	987	U89922	lymphotoxin beta (TNF superfamily, member 3)	0 081431989	0.705262065	1.14225E-05	0.069803458	0.012069263	5.95219E-05
W52493_at	1013	W52493		4.17744E-05	0.407939223	0.47764998	2.61848E-05	0.001311163	0.165780725
X06318_at	1048	X06318	protein kinase C, beta 1	4.53981E-05	0.309598889	0.000193355	0.01564851	0.739435449	0.033561473
X07315_at	1053	X07315	nuclear transport factor 2 (placental protein 15)	0.00096734	0.024484461	0.000991289	0.558914618	0.994799819	0.56276584
X14008_rna1_f_at	1056	X14008	lysozyme (renal amyloidosis)	0.047298803	0.921767172	1.2563E-05	0.081015792	0.023720356	0.000192698
X14046_at	1057	X14046	CD37 antigen	0.032116442	0.896768704	6.54708E-06	0.097237805	0.024859085	0.000287679
X14830_at	1058	X14830	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	0 936178672	0 000286907	0.137976127	0.000630986	0.183095639	0.024428637
X16316_at	1059	X16316	vav 1 oncogene	0.005646314	0.4794965	0.000157845	0.002861938	0.337620027	0.00013174
X54870_at	1065	X54870	DNA segment on chromosome 12 (unique) 2489 expressed sequence	0 000450913	0.241248516	0.00029577	0.07293822	0.916408	0.059393045
X58529_at	1070	X58529	immunoglobulin heavy constant mu	0 026942297	0.975028968	5 32141E-08	0.070184957	0.002196974	6 90925E-06
X60673_s_at	1072	X60673	adenylate kinase 3	0.014055428	1.64563E-05	0.000854329	0.036097108	0.40449053	0.17235001
X63741_s_at	1074	X63741	early growth response 3	0.050166995	0.302932401	1.63652E-08	0.522269647	0.000467351	0.000208487
X66358_at	1079	X66358	cyclin-dependent kinase-like 1 (CDC2-related kinase)	3.6744E-05	0.079324094	3.35901E-05	0.080441339	0.984409054	0.077518373
X66839_at	1080	X66839	carbonic anhydrase IX	3.93574E-06	0.662915937	0.008885816	0.000624117	0.057988735	0.078713562
X68277_at	1082	X68277	dual specificity phosphatase 1	0.003463894	0.023542489	5.00933E-13	0.79747022	4.48312E-05	0.000125081
X72882_at	1084	X72882		0.000586574	1.73881E-05	0.061863645	0.20511364	0.136254698	0.010057929
X75962_at	1085	X75962	hypothetical protein FLJ10747,tumor necrosis factor receptor superfamily, member 4	1 07753E-05	0.259082214	0.000322398	2 07333E-06	0.445393473	4.56511E-05
X83705_s_at	1089	X83705	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	0.000211219	0.000641028	0.003169595	0.843987656	0.474177301	0.409652768
X96584_at	1096	X96584	nephroblastoma overexpressed gene	0.000449835	0.36091834	0.013539811	0.00014621	0.323949108	0.003364493
X99142_at	1097	X99142	keratin, hair, basic, 6 (monilethrix)	0.104620098	0.022019682	0.075077447	0.00038452	0.881497721	0.000232112
Y07595_at	1099	Y07595	general transcription factor IIH, polypeptide 4 (52kD subunit)	0 000268402	0.028695565	5.26844E-05	0.352269642	0.704788647	0.206775434
Y09022_at	1102	Y09022	Not56 (D. melanogaster)-like protein	0.000142024	0.084289616	0 000108418	0 131801466	0.949831739	0.118236485
Z35093_at	1105	Z35093	surfeit 1	0.000740458	0.015177247	0.000173743	0.635076989	0.718277145	0.428942461

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Table 7

	Prostatic tissues	Cell Line			
		BRF-55T	PZ-HPV7	BPH-1	LNCaP
Up-regulated genes	61	33	22	20	20
Down-regulated genes	43	31	28	30	33
Total	104	64	50	50	53